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Exhibit 1

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA

molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

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The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-739. The polypeptides sequences are designated SEQ ID NO: 740-1478. The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-739 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-739. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-739 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-739. The sequence information can be a segment of any one of SEQ ID NO:1-739 that uniquely identifies or represents the sequence information of SEQ ID NO:1-739.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

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This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-739 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-739 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-739; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-739; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO: 1-739. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-739; (b) a nucleotide sequence encoding any one of the

amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

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The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-739; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein,

and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

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The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The

invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

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The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products.

Compounds and other substances can effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

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4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

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The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid

which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

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The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-739. The sequence information can be a segment of any one of SEQ ID NO:1-739 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-739. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-

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mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4²⁰ possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3×25) . The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to

naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

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The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophobicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

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The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

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The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134

-143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

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The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligon), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences.

Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment,

by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

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The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

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Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing. The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-739; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:740-1478; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEO ID NO:740-1478. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-739; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO: 740-1478. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptorlike polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification

and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-739 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-739 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO:1-739 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

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The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-739, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-739, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-739 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

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The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-739, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the

nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

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In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-739, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide.

In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-739 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-739 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

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Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include E. coli, Bacillus subtilis, Salmonella typhimurium and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example,

pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

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Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-739, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:740-1478 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-739 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding

region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-739, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxyaminomethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine,

pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a

2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

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In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-739). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to

allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

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PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance

their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

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The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If

linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

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Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a

suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations

of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

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The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

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The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:740-1478 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-739 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-739 or (b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NO:740-1478 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:740-1478 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:740-1478.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the

disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

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Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein

which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

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The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models

that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:740-1478.

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The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other

immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

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The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

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The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTN, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST

(Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

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The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into

pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e,g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states

involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

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Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression

by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences.

Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a

tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

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4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in

disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

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Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

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The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

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The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of

course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or ago of the binding interaction.

Any or all of these research utilities are capable of being developed into reager grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

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Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of therapeutic

compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

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Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John

Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

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A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for reengineering damaged or diseased tissues, transplantation, manufacture of biopharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

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Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune

disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

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Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds*. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

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A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, 10 Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994. 15

4.10.6 TISSUE GROWTH ACTIVITY

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A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative

disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

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Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager

syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

25 International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J.

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4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the

polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

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Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a

subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

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Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or

eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

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Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology

154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may

also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

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4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the

migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al.,

Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991);

Schaub, Prostaglandins 35:467-474, 1988.

4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a

polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

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Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of

tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

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The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog), Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin, Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in

Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

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A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those

described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek,
D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and
Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static
conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987;
Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,
Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

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4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3)

combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

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The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves.

Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity

of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

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The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins

involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

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Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not

limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

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Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
- (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
- (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

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- (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
 - (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody

binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

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A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related

diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

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The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences

of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

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4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods.

Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01µg/kg to 100 mg/kg of body weight, with the preferred dose being about 0.1µg/kg to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

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4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity

of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers

to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

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In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When coadministered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factors, thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or

cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

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Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the

pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

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When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art.

Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

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Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon

dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

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A pharmaceutical carrier for the hydrophobic compounds of the invention is a cosolvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological

effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

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The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each

individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

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The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure

proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

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A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients

of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

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Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating

concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

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A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD_{50} and ED_{50} . Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%.

In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

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4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab} , and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain.

Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

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An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 4, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

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5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A. synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide

primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a

fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or

survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

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Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol., 133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures

such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a nonimmunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

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5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536

(1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

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Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, <u>J. Mol. Biol., 227</u>:381 (1991); Marks et al., <u>J. Mol. Biol., 222</u>:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely

inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

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Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to

prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 Fab Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_{v} fragments.

5.13.5 Bispecific Antibodies

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Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

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Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan).

Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

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Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., <u>J. Immunol.</u> 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody

homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., <u>Proc. Natl. Acad. Sci. USA</u> 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., <u>J. Immunol.</u> 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991). Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

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5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in

vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

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5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin,

crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

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In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to

create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

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A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-739 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-739 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

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As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for

commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

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4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

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In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein

spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

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5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three applications designated PHRED, PHRAP, and CONSED. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-739 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 120, gb pri 120, UniGene version 120, and Genpept 120) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 120, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and

extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

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4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of

the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-739, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

 In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to activity observed in the absence of the compound). Alternatively, compounds

identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

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The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or

can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-739. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-739 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection

of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

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Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers.

Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

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Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M

1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

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Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6,

incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected N-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

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The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease CviJI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (CviJI**), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald et al. (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a CviJI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that CviJI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

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Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate

(all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane. Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

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5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were

spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

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5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. Chromatograms were base called and assembled using a software suite from University of Washington, Seattle containing three applications designated PHRED, PHRAP, and CONSED. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-739 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 120, gb pri 120, UniGene version 120, and Genpept 120) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

The nearest neighbor result for the assembled contig was obtained by a FASTA version 3 search against Genpept release 120, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for each assemblage from Genpept (and

contains the translated amino acid sequences for which the assemblage encodes). The nearest neighbor results for SEQ ID NO: 1-739 are shown in Table 2.

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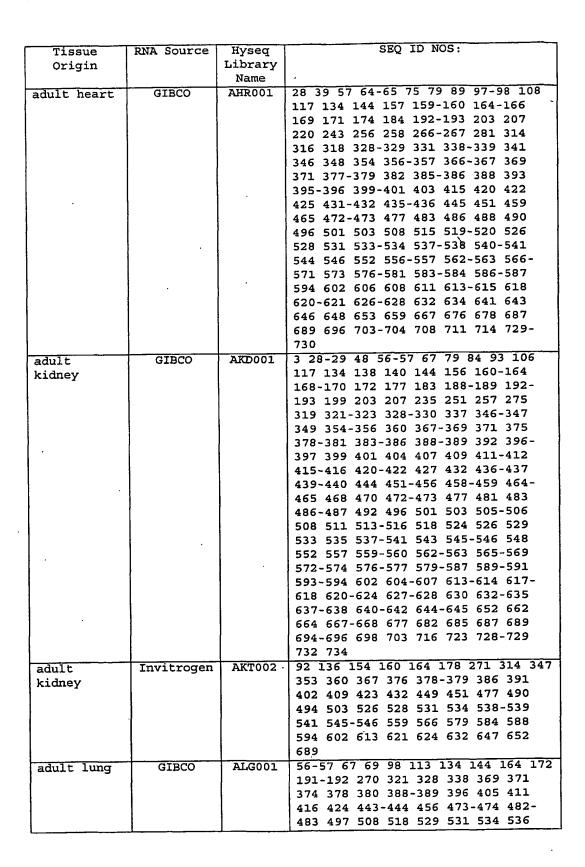
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Tables 1, 2, and 3 follow. Table 1 shows the various tissue sources of SEQ ID NO: 1-739. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homologue for each assemblage and contains the translated amino acid sequences for which the assemblage encodes. Table 2 also shows homologues with identifiable functions for SEQ ID NO: 1-739. The polypeptides were predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of translated novel polynucleotides to known polynucleotides (W.R. Pearson, Methods in Enzymology, Vol. 183: pp. 63-98, (1990), herein incorporated by reference). Table 3 shows the predicted amino acid sequence corresponding to the novel nucleic acid contig sequences.

Table 1 - Tissue Sources

Tissue	RNA Source	Hyseq	SEQ ID NOS:
Origin		Library	
		Name	
adult brain	GIBCO	AB3001	28 46 54 62 95 117 134 175 188-189
[324 330 337 356 369 371 378 386
			389 396 432 435-436 468 472-473
			476-477 483 486 518 538-539 543
			545 557 565 571 573 578 582 598
·			613-614 619 627 632 634 639 687
İ			709
adult brain	GIBCO	ABD003	5 12 46 52 57 66 79 91 97 134 144
		,	148 150 162 164 172 175-176 181
	;		186 193 250 323 325-327 330 334
			338 362 367 369 371 378-379 386
			388-389 392 396-397 399-401 403
}	}		416 422 435 444 449 451 454 461
			463-464 468 472-473 483 486 494
ĺ			506 511 513 516 520 523-524 526
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Genomic	Genomic	EPM003	43 164 295
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fetal brain	Clontech	FBRs03	444 587
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fetal heart	Invitrogen	FHR001	57 75 164 547
fetal	Clontech	FKD001	57 164 172 179 188 194 208 218 230
kidney			240 250 330 334 369 388 401 413
			439 454 465 529 546 550 573 576
			581 583 594-596 602 634 648 667
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fetal	Clontech	FKD002	2 560
kidney		_	
fetal	Invitrogen	FKD007	565 596-597
kidney			
fetal lung	Clontech	FLG001	75 164 355 386 428 455 513 524 528
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fetal lung	Invitrogen	FLG003	30 157 162 169 188 243 253 256 283
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liver-	University		65 67 70 74-77 79-80 84-87 89 92
spleen			96 98-100 104 117 122-130 138 140
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liver-	University		
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fetal liver	Invitrogen	FLV001	3 27 35 48 50 56-57 66 75 92 94
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		1	243 272 324 328 333 335 353 369-
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fetal liver	Clontech	FLV002	343
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muscle	-	1	341 352 380 389 402 407 444 464
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macrophage	Invitrogen		28 46 56-57 59 67 75 78 109 117
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brain	University		472 506 513 523 531 534 580 615
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			369 371 378-379 382 388-389 392
			396-397 400-402 405 415-416 420
			422 429 432 435-436 443-444 449
			454-455 457-459 465 479 481-486
			491 497 501 503-504 506 508 511
			1
			514 516 520 523-525 529 532-533
			535 538-539 545 548 552-554 556
			559-560 562-563 565-566 569 571-
			573 576 579 581 585-587 590 593-
			594 598 600-602 604 606-609 613-
			614 618 620-622 624 627 630 632-
			634 636 638 643 645 660-662 667
			678 682 684 686 689 691 693 696-
			698 714 726
leukocyte	Clontech	LUC003	11 54 97 152 164 330 479 546 564-
1 -		,	565 593 613 627 634 646 696 729
melanoma	Clontech	MEL004	2 57 67 79 164 171-173 188 193 196
from cell	1		232 321 337 341 346 367 379-380
line ATCC			388 407 427 454 472 477 482 501
#CRL 1424		i	520 539 545 552 556 579 588 593
WORLD TARK			598 611 621 631 648 665 714 730
	Invitrogen	MMG001	3 20-21 29 31 54 56-57 63-66 79 94
mammary	Invictogen	raidool	109 112-113 117 122 125 138 141
gland			154 160 162 164 172 176 186 189
			192 204 214 220-221 232 238 251
			1 11 2 2 2 2
		ł	255 257 273 276-278 324 326 328-
			331 333 335 337 341-343 347 354-
			355 357 367-371 374-375 379 382-
	1		386 388-392 397 399-400 404 406-
1	}	\	408 410-411 425 431 435-436 444
			451 455 457 459 461 464-465 470-
	1		471 475 479 483 485 487-488 491
			501 506-508 511 513-519 523-524
	1		526 529 531-532 534-535 537 539-
		[540 542-545 552-554 557-560 563
	1	1	566 569 572 577 580 584 587-588
	1		590 597-598 602 604-605 609 611
		1	613 615 624 627 631-634 637 639-
			640 643 648-649 654 664 669-670
			672-673 676-679 681 689 691-695
			697-698 706 714 731 734 737

			CEO TO YOU
Tissue	RNA Source	Hyseq	SEQ ID NOS:
Origin		Library	
		Name	
induced	Strategene	NTD001	36 57 164 284 388 397 420 481 485
neuron			501 524 528-529 539 542 545 560
cells		,	571 579 582 595 602 620 637 654
			667 689 730
retinoid	Strategene	NTR001	524 584 693
acid			
induced			
neuronal		ļ	
cells			
neuronal	Strategene	NTU001	36-38 120 204 331 351 354 357 386
cells	Condogonio		388 399 411 442 459 516 533 539
CCITS			545 565 586 606 615 621 637-638
			642 646 648 714 730
-1	Clontech	PLA003	503 579 690
placenta		PRT001	15 40 65 164 187 207 229 337 348
prostate	Clontech	PRIOUI	367 375 377-378 395 406 416 428
		İ	458 468 476 511 524 526 531 534
			538 555 559 563 576 584 597 613
			622 624 631 642 667 672 677 684
			724 734
rectum	Invitrogen	REC001	57 67 164 260 331 343 370-371 380
		}	382 384 404 409 436 444 475 485
1			498 513 524 526 540 542 552 554
			581 615 619 624 627 634 654 659
1			671 689 714
salivary	Clontech	SAL001	21 84 106-107 152 179 238 246 255
gland			273 287 371 378 383 401 407 420
, -			455 475 477 509 512 515 521 541
			548 565 570-571 573-574 589 606
			628 634 636 652 689 703 738
skin	ATCC	SFB002	192
fibroblast			
skin			
fibroblast	I ATCC	SFB003	464
	ATCC	SFB003	464
small	Clontech	SFB003	57 66 71 98 116 150 164 172 327
			57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401-
small			57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528
small			57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678
small intestine	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711
small intestine skeletal			57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 .
small intestine	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 . 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552
small intestine	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 . 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738
small intestine	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648 659 688-689 691 693 695
small intestine skeletal muscle	Clontech	SIN001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648
small intestine skeletal muscle spinal cord	Clontech	SKM001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648 659 688-689 691 693 695
small intestine skeletal muscle spinal cord	Clontech	SKM001	57 66 71 98 116 150 164 172 327 336 343 362 367 379 388 397 401- 402 417 429 433 436 496 526 528 533 590 602 620 631 634 667 678 711 3 57 66 101 164 172 256 266 325 379 385 449 468 485 487 518 552 554 566-567 570 582 584 590 606 611 628 631 738 10 54 57 66 75 100 102 114 144 164 175 193 199 215-216 325 334 337 367 370 380 385-386 406 411-413 419 429 466 470 486 518 526 529 531 534 574 579 585 587 590 604 620-621 631-632 634 642 644 648 659 688-689 691 693 695

Tissue	RNA Source	Urraca	SEQ ID NOS:
	RNA Source	Hyseq Library	SEQ ID NOS.
Origin		Name	
		Name	485 526 532 569 576 579 581 586
			603 631 634 677 682 689
			_ ·
thalamus	Clontech	THA002	17 31 57 66 109 127 164 217-218
			262 315-316 324 330 357 369 386
			388 400 406 435 456 459 464 468-
	,		469 515-516 537 540-541 556 566
	, i		574 590 611 622 631 634 644 648
		٠.	656 677~678 680
thymus	Clontech	THM001	6 15 26 54 79 164 172 187 193 201
			264 291 315 329 331 351 356 367
			397-398 401 407 412 424 427 429
			435-436 443 451 474 478 482 549
			563 565 567 569 576 578 581-582
			610 615 621 631-632 634 648 662
			667 669 679 689 693 696
thymus	Clontech	THMc02	3-6 8 11 16 18 34 58-59 67 132 149
011700			162 164 167 172-173 186 188-189
			193 200 203 216 223 232 239 255
	}		263 265 319-320 331 333-334 355
			359 370 373 377-380 382 387-390
			393 395 398-399 402 404 408 420
			427 434 436 467 475-476 503 508
			518 524 526 532 540 560 563 565
			571-572 576-577 579 582 598 601
			603 612-613 615 621 627 632 634
			639 641 648 651 657 659 662 672
			677-678 684-686 689 696 699 706
	<u> </u>		714-716 722 726-729 732
thyroid	Clontech	THR001	5 29-30 40 54 57 66 72 79 117 144
gland]	160 164 166 170 172 176 183 188-
			189 208-209 219 230 285-286 314
]	318 327 331 335 338 344 347 354
			363 367 375 377-380 382 384-386
ļ	1	į	388 393 397 399 401-403 419 422
			429 436 442 444 451 456 458-461
			464 467-468 470 472-473 476-477
			481 488 494 503 508-509 511 516
			519-521 524 528-529 533 537-538
į			543 548 557 559-560 563 565-566
		İ	571-574 576 582 585 587 590-591
1			593-594 596-597 606 614-615 620-
]	1	621 623-624 627 631-634 640 650-
		ĺ	651 653 662 667 669-670 675 679
			689 708 712 714
traches	Clontech	TRC001	156 164 171 240 375 378 390 400
trachea	CTOHCECH	IRCOOL	422 468 484 565 574 581 585 587
		1	631 654 689 714
	01	700000	
uterus	Clontech	UTROOL	65. 77 79 101 164 220 367 369 451
			468 526 530 533 548 554 559 562
ľ		<u> </u>	568 573 582 594 637 648 689

Table 2 - Nearest Neighbor Results

SEQ SEQ Accesting Section					Description	Smith	*
NO: NO: NO: NO: NO: NO: NO: NO: NO: NO:	SEQ	SEQ	Acces-	Species	Description	SILLCII	
No.						Water	identity
USSN 09/48 8,725 1 1000 gi70214 Mus musculus secretory carrier membrane protein 4 4 4 4 4 4 4 4 4 4	NO:		No.				
1 1000 1001 1000 100	1						
8,725 1 1000 gi70214 Mus musculus secretory carrier membrane protein 4 2 10017 R06463 Homo sapiens Derived protein 6 Clone ICAl3 (ATC 40553) Stmilar to other protein phosphatases 1, 2A and 2B 1, 2A and 2B 2 2 2 2 2 2 2 2 2					1	score	
1 1000 gi70214 Mus musculus secretory carrier membrane protein 4 2 10017 R06463 Homo sapiens Derived protein of clone ICA13 (ATC 40553). 3 10020 gi10659 Caenorhabditis elegans Similar to other protein phosphatases 1, 2A and 2B Human secreted protein phosphatases 1, 2A and 2B Human secreted protein phosphatases 1, 2A and 2B Human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human secreted protein human							
1000 1702 1001 1000		8,725					
Membrane Protein 4	1	1000		Mus musculus		567	85
2 10017 R06463 Homo sapiens Derived protein 4 S48 protein of clone ICA13 (ATCC 40553). 36 10020 gi10659 Caenorhabditis elegans Similar to other protein phosphatases 1, 2A and 2B 24 10024 G03460 Homo sapiens Human secreted protein, Similar to other protein phosphatases 1, 2A and 2B 325 36 36 36 36 36 36 36 3			84				
10017 R06463 Homo sapiens Derived protein of clone ICA13 (ATCC 40553). 3 10020 gi10659 Gaenorhabditis elegans of chore protein phosphatases 1, 2A and 2B Homo sapiens Homan secreted protein phosphatases 1, 2A and 2B Homo sapiens Homan secreted protein Homan secreted protein Homan lung tumour protein SAL-25 1st predicted amino acid sequence. Homo sapiens Homan lung town protein SAL-25 1st predicted amino acid sequence Homo sapiens Homo							1
10017 Rose					•		
Clone ICA13 (ATCC 40553).	2	10017	R06463	Homo sapiens		848	100
(ATCC 40553) Similar to S						\ \ \	1
10020 gi10659 Caenorhab-ditis elegans Similar to other protein phosphatases 1, 2A and 2B						ļ	
10020 67 ditis elegans other protein phosphatases 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2A and 2B 1, 2A and 2B 1, 2A and 2B and 2B 1, 2A and 2B and 2B 1, 2		ļ			(ATCC 40553).		
10024 G03460 Homo sapiens Human secreted protein, Human secreted protein, Human secreted protein Human secreted protein Human secreted protein Human secreted protein Human secreted protein Human secreted protein Human secreted protein Human lung tumour protein SAL-25 lst predicted amino acid sequence. Human alpha-2-delta-D polypeptide from splice variant 1. Human secreted protein Human alpha-2-delta-D polypeptide from splice variant 1. Human secreted protein Human alpha-2-delta-D polypeptide from splice variant 1. Human secreted protein Human alpha-2-delta-D polypeptide from splice variant 1. Human secreted protein Hu	3	10020	gi10659	Caenorhab-	similar to	325	36
1, 2A and 2B		!	67	ditis elegans	other protein]
10024 G03460 Homo sapiens Human secreted protein, Secreted protein Secreted protein, Secreted protein Secreted protein, Secreted protein Secreted protein Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein salion Secreted protein Secreted protein Secreted protein salion Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secretal protein					phosphatases		
10022 S03400 Solution Sapiens Secreted Secr		i]		1, 2A and 2B	İ	
Secreted protein, Secreted protein, Secreted protein, Human 5' EST secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted Secreted Secreted Secreted protein Secreted protein Secreted	4	10024	G03460	Homo sapiens	Human	439	98
Tool	•				secreted	ļ	
10032 112303 11		·			protein,	İ	
Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted protein Secreted Secre		10032	V12505	Homo sapiens	Human 5' EST	136	87
Protein Protein Final	,	10032	112303	2200 Dup-0133		İ	1
10042 Y29511 Homo sapiens Human lung tumour protein SAL-25 lst predicted amino acid sequence. 7							
tumour protein SAL-25 1st predicted amino acid sequence. 7 1006 Y92324 Homo sapiens Human alpha- 2-delta-D polypeptide from splice variant 1. 8 10064 gi45893 Homo sapiens Gab2 425 58 9 1007 gi70183 Homo sapiens Gab2 151 75 10 1008 gi89606 Homo sapiens 5 protein that is immuno- reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo- protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54		10042	V29511	Homo saniens		701	100
SAL-25 1st predicted amino acid sequence. 7	0	10042	123311	nomo sapreme			
Predicted amino acid sequence.	•	1]				
amino acid sequence.			'			ļ	
Sequence Sequence		ł	ì			1	1
Toole		1	1		}		
2-delta-D polypeptide from splice variant 1. 8 10064 gi45893 Homo sapiens Gab2 425 58 9 1007 gi70183 Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus CAMP-specific 223 54		1006	V92224	Homo caniens		763	100
B 10064 gi45893 Homo sapiens Gab2 425 58	′	1008	192324	nomo sapiens			
### From splice variant 1. ### 10064		1				Ì	
Variant 1.		1		· .		İ	
8 10064 gi45893 Homo sapiens Gab2 425 58 9 1007 gi70183 Homo sapiens 98 10 1008 gi89606 Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus CAMP-specific 223 54		Į.	}			ł	1
9 1007 gi70183 Homo sapiens 9 1008 gi89606 Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54			1 45000	Wana gamiang		425	58
9 1007 gi70183 Homo sapiens protein that 1226 99 10 1008 gi89606 Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54	8	10064	, -	TOUG Sabrens	Jabe	1 22	
98 1007 988 1008 gi89606 Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54		 		Ylone design		151	75
10 1008 gi89606 Homo sapiens protein that is immuno-reactive with anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54	9	1007	_	nomo sapiens		-3-	'
11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54		1.000		Vome deniene	protein that	1226	99
Teactive with anti-PTH polyclonal antibodies 11	10	1008	, -	nomo sapiens	1 -	1. 1220	-
anti-PTH polyclonal antibodies 11 10088 gi37792 Homo sapiens Metallo-protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54			•				
11 10088 gi37792 Homo sapiens Metallo- 1512 98 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus CAMP-specific 223 54				1			
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11 10088 gi37792 Homo sapiens Metallo- protease 1 12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54			1				1
11 10088 9137792 Homo sapiens protease 1 12 10089 9129472 Homo sapiens membrane associated guanylate kinase 2 13 10091 9133478 Mus musculus cAMP-specific 223 54			<u> </u>			1 1 5 1 2	- 00
12 10089 gi29472 Homo sapiens membrane associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54	11	10088	1 -	Homo sapiens		1512	1 36
32 associated guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54					1 -		100
guanylate kinase 2 13 10091 gi33478 Mus musculus cAMP-specific 223 54	12	10089	1 -	Homo sapiens	1	523	100
		1	32				
13 10091 gi33478 Mus musculus cAMP-specific 223 54					, -		1 *
13 10091 9133478 Mus musculus Cran December 13			_		1		
	13	10091	gi33478	Mus musculus		223	54
	1		63		cyclic		<u></u>

CTO .	SEQ	Acces-	Species	Description	Smith	*
SEQ ID	ID	sion	species	Description	-	Identity
NO:	NO:	No.			Water	
NO.	in	1.0.			man	İ
	USSN				Score	
	09/48				1	
	8,725		,		1	
				nucleotide		
	ŀ			phosphodi-		
				esterase PDE8;	ļ	
	1			MMPDE8		
14	10098	gi69793	Homo sapiens	cysteine-rich	1068	100
	1	11		repeat-	Į.	
				containing		
				protein S52		
				precursor		
15	10102	G01395	Homo sapiens	Human	297	88
		1		secreted		
	1	, 05.453	5-1-1	protein, casein kinase	293	84
16	10103	gi85473	Rattus	1 gamma 1	293	U-3
		3	norvegicus	isoform	j	
17	10104	Y60017	Homo sapiens	Human	154	100
			_	endometrium	1	
ł				tumour EST		İ
1				encoded		
ļ				protein 77.		
18	10108	G03290	Homo sapiens	Human	215	97
	1	Í		secreted		i i
			<u> </u>	protein,		
19	10110	gi72922	Drosophila	CG1271 gene	208	46
	<u> </u>	99	melanogaster	product	822	89
20	10111	gi45123	Rattus	Co /colmodulin	822	69
ĺ	1	34	norvegicus	Ca/calmodulin- dependent		1
1	ļ			protein kinase	ļ	
				kinase alpha,	1	
				CaM-kinase		,
Ì		j		kinase alpha	1	
21	10113	Y41694	Homo sapiens	Human PRO382	633	97
				protein	1	
		1		sequence.		
22	10114	gi34907	Rattus	calmodulin-	531	99
		5	norvegicus	binding	}	
		1		protein		
23	10116	gi16298	Bos taurus	endozepine-	937	87
		1		related		
1				protein		
L		<u> </u>		precursor		
24	10121	gi89797	Canis	Band4.1-like5	643	100
		43	familiaris	protein	602	100
25	10126	Y99420	Homo sapiens	Human PRO1486	607	100
				(UNQ755) amino	1	
	I		Home ganiana	acid sequence protein	614	73
26	1013	gi80475	Homo sapiens	tyrosine	014	, ,
	ــــــــــــــــــــــــــــــــــــــ	0	L	- cyrosine	J	<u> </u>

CEO	TSEO	Acces-	Species	Description	Smith	
SEQ	ID	sion	species	Description	Suiten	Identity
NO:	NO:	No.			Water	racinetes
NO.	in	NO.			man	
	USSN				Score	
	09/48					
ļ	8,725				1	
	-7:			phosphatase		
27	10136	W02105	Homo sapiens	Human L-	1243	98
	İ			asparaginase.		
28	10142	Y35924	Homo sapiens	Extended	862	89
				human secreted	ļ	
				protein		
			******	sequence,	329	98
29	10148	gi33349 82	Homo sapiens	R27216_1		
30	1015	G02485	Homo sapiens	Human	120	72
				secreted		
				protein,	2607	98
31	10154	gi10798 804	Homo sapiens	sperm antigen	2607	98
32	10175	Y96864	Homo sapiens	SEQ. ID. 37	536	100
		[from		
	l			WO0034474.		
33	10196	gi55362 1	Homo sapiens	profilaggrin	346	39
34	10198	gi14190	Mus musculus	odorant	281	53
		16	l	receptor		
35	10200	Y57903	Homo sapiens	Human	448	100
				transmembrane		į
	1			protein HTMPN-		
36	10208	gi40624	Escherichia	21.	505	100
36	10208	92	coli		303	100
37	10212	gi88252	Escherichia	ORF f141	625	96
"	1	9	coli			
38	10213	gi40627	Escherichia	Hypothetical	773	98
ļ		78	coli	protein HI0761		
39	10214	gi66938	Rattus	opioid growth	661	44
		32	norvegicus	factor		
	<u> </u>			receptor		
40	10227	G01360	Homo sapiens	Human	384	100
			1	secreted protein,		
<u></u>	10236	gi16512	Escherichia	brocern,	373	100
41	10236	57	coli	•	3/3	100
42	10241	gi27692	Escherichia	catabolite	178	96
""		62	coli	gene activator		
				protein		
43	10245	gi17895	Escherichia	orf,	679	98
		39	coli	hypothetical		
1				protein		
44	10246	gi88249	Escherichia	ORF_0179	488	97
<u></u>	<u> </u>	2	coli			
45	10247	gi17421	Escherichia	Sn-glycerol-	323	100
	l	49	coli	3-phosphate	L	<u></u>

				Decemination	Smith	&
SEQ	SEQ	Acces-	Species	Description	SILLCII	Identity
ID	ID	sion			Water	Identity
NO:	NO:	No.			man	
	in USSN			•	Score	
	055N 09/48			•	00010	i
1	8,725					
	0,723			transport		
				system	İ	
				permease		
i				protein UgpA.]
46	10282	Y29817	Homo sapiens	Human synapse	521	96
			_	related	!	
Ì				glycoprotein		
				2.	· · · · · ·	
47	1031	gi64351	Mus musculus	putative E1-	990	86
ļ	}	30		E2 ATPase	<u> </u>	
48	1040	gi85412	Homo sapiens	Human giant	471	63
		4		larvae		
l .	i			homologue		
49	1043	gi38822	Homo sapiens	KIAA0782	154	61
<u> </u>		85		protein		
50	1051	gi17821	Homo sapiens	anion	172	100
		6		exchange	1	}
				protein 1	100	92
51	1053	Y76748	Homo sapiens	Human protein	180	92
]				kinase		
				homologue, PKH-1.		}
<u></u>	1000		Mus musculus	ADAM 4	492	65
52	1062	gi96501 4	Mus muscurus	protein	472	
		4		precursor		
53	1063	gi23938	Drosophila	A-kinase	580	60
33	1003	80	melanogaster	anchor protein		
				DAKAP550	1	ļ
54	1066	gi27467	Caenorhabditi	contains	607	35
-		88	s elegans	similarity to		
	1			transacylases		
55	107	G00357	Homo sapiens	Human	183	77
				secreted		
1				protein,		`
56	1071	gi91059		Acetylgluta-	505	36
l'		37	fastidiosa	mate kinase		
57	1085	R95913	Homo sapiens	Neural thread	257	55
				protein.	<u> </u>	
58	1086	Y76332	Homo sapiens	Fragment of	387	58
				human secreted		
1				protein		
				encoded by		1
	1	1		gene 38.	873	99
59	1088	gi45896	Homo sapiens	·KIAA0999	0/3	33
	 	42		protein	360	85
60	109	gi76343	Homo sapiens	KIAA0999 protein	300	35
	1.005	1 204007	Homo sapiens	Human	701	97
61	1095	Y94907	uomo sabiens	secreted	1 ,31	1
L		<u> </u>		1202000	<u> </u>	

_===			G	Documention	Smith	8
SEQ	SEQ	Acces-	Species	Description	Smith	Identity
ID	ID	sion No.			Water	Identity
NO:	NO: in	NO.			man	
	USSN				Score	
	09/48			•	50020	
	8,725]	
	07.23			protein clone		
İ				ca106 19x		
				protein		
				sequence		
62	1102	Y07096	Homo sapiens	Colon cancer	1982	100
				associated		1
				antigen	\	
				precursor	`	
				sequence.		
63	1105	Y84907	Homo sapiens	A human	983	91
				proliferation		
1	1	(and apoptosis related	Î	
		1		protein.	ŀ]
64	1108	gi13989	Mus musculus	Ca2+	1307	89
04	1108	03	rids musculus	dependent		
		03	•	activator		
Ì			*	protein for]
ĺ				secretion		
65	1109	Y91524	Homo sapiens	Human	2400	99
				secreted		
l .				protein		
		i		sequence		
		1		encoded by	ł	
l				gene 74		
66	1113	gi16574	Sus scrofa	calcium/cal-	1348	94
1		62		modulin-		
				dependent		
ļ		1	·	protein kinase II isoform		
1		1		gamma-E		
67	1117	Y32169	Homo sapiens	Human growth-	2831	97
"'		132109	1101110 Dapteris	associated		-
				protease		
				inhibitor]
1.				heavy chain		
				precursor.		
68	1118	gi30635 17	Homo sapiens		1138	98
69	1125	gi82482	Homo sapiens	sphingosine	1290	98
		.85		kinase type 2		
J				isoform		
70	1132	Y94918	Homo sapiens	Human	437	59
1				secreted		
				protein clone		
	1			dd504_18]
				protein	1	
	1,11	G: 4500C	Vomo coniona	sequence prepro-major	209	40
71	1143	gi45806	Homo sapiens	Prepro-malor	203	1

SEQ SEQ Acces- ID ID sion NO: NO: No.	Description Smith % - Identity
NO: NO: No.	_ _ _
i lin i i	man
	Score
USSN	score
09/48	
8,725	- la - la - mato in
77	basic protein
	homolog 131 87
72 1146 gi18239 Homo sapier	
5 .	adhesion
	kinase ns Human CSGP-2 931 100
73 1161 W90962 Homo sapier	
	protein. 159 93
74 117 W69428 Homo sapi	
	secreted
	protein
	bp537_4.
75 1170 gi34339 Homo sapi	
76 1175 gi79602 Homo sapie	Payaran
43	kinase SNAK
77 118 gi53600 Homo sapie	
93	antigen
78 1183 gi29203 Homo sapie	
7	helix
	phosphoprotein
79 1193 gil8991 Rattus	polysialyltran 171 76
86 norvegicus	sferase
80 1195 gi13994 Homo sapie	
62	nine-protein
	kinase PRP4h
81 1198 gi18153 Homo sapie	
5	precursor
82 1201 gi56689 Rattus	plasma 244 73
35 norvegicus	membrane Ca2+
	ATPase isoform
	1kb
83 1207 gi62248 Homo sapie	
68	kinase TBK1
84 1210 gil7964 Homo sapie	
6	component Cls
85 1211 gi14831 Homo sapie	ns 296 65
87	
86 1214 gi78006 Streptococ	
38 pneumoniae	
87 123 Y44810 Homo sapie	
	Aspartic
	Protease-2
	(NHAP-2).
88 1259 gi21166 Homo sapie	ns EAR-1r 128 70
72	
89 1266 gi72431 Homo sapie	
25	protein
90 1270 gi12894 Homo sapie	
45	kinase epsilon
	DGK

SEQ	SEQ	Acces-	Species	Description	Smith	*
ID	ID	sion	opecies	Societa	-	Identity
	NO:	No.			Water	
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İ	in		•		Score	
[USSN	ĺ			Score	
ļ	09/48					
1	8,725					
91	1290	gi14293	Drosophila	ubiquitin-	470	41
1		71	melanogaster	specific	-	
1				protease	1	
92	1291	Y66755	Homo sapiens	Membrane-bound	993	100
92	1291	100/33	nome captain	protein		
ļ				PRO1185.	,	
					1103	99
93	1296	gi96520	Homo sapiens	scavenger	1183	99
		87		receptor		
į		1	•	cysteine-rich	1	
				type 1 protein	1	
				M160	l	
				precursor	1	
94	1299	gi73003	Drosophila	CG7683 gene	397	40
34	1233	98	melanogaster	product]	
			Rattus	CL1AA	216	100
95	1317	gi36951		CLIAA	210	100
		15	norvegicus			
96	132	gi18717	Homo sapiens	12-	176	97
		1		lipoxygenase		
97	1330	Y12482	Homo sapiens	Human 5' EST	65	44
			_	secreted		
	ì			protein	1	
98	1336	qi10798	Homo sapiens	MLTK-beta	2366	99
90	1 1330	814	nomo bapreno			
- 00	135	gi45609	Homo sapiens	effector cell	190	74
99	135	-	HOMO Saprens	protease	130] '-
	ĺ	0		. –	1	
				receptor 1	<u> </u>	
100	1356	gi19305	Mus musculus	envelope	131	36
ŀ	l	7	}	polyprotein		
ŀ		j		precursor		
101	1369	gi45865	Homo sapiens	glucocorticoid	596	89
		7	_	receptor		ļ
ì	ł	Ì		alpha-2	{	[
102	1392	gi84935	Mus musculus	nuclear	145	59
102	1374	1 -	L'us muscurus	localization	-10	
J]	19	1	1	1 .	
١.		1	1	signal binding	1	['
		<u> </u>		protein		
103	1408	gi31270	Rattus '	potassium	176	84
l	1	51	norvegicus	channel		1
	}	1	1	regulatory	ŀ	1
		1		protein KChAP		
104	141	gi64536	Mus musculus	putative	204	33
104	141	13		protein kinase	1	
		1	Home continue	neuropathy	769	100
105	1424	gi29825	Homo sapiens		, 09	100
		01		target	1 .	
1		,		esterase	_	<u> </u>
106	143	W50033	Homo sapiens	Human immunity	1201	98
		1	_	related		
1				factor.	}	
107	1431	gi10644	Heterodera	hypothetical	133	36
1 -0/	1.131	1300-3	1	1 1 &		

ero l	SEQ	Acces-	Species	Description	Smith	*
SEQ ID	ID	sion	species	peacriperon	-	Identity
		No.			Water	racincity
NO:	NO:	NO.			man	
	in		, , , , , , , , , , , , , , , , , , ,		Score	
	USSN				2016	
	09/48					
	8,725					
		565	glycines	esophageal		
		ł		gland cell		
			ļ 1	secretory		
				protein 10		
108	1441	gi30440	Myxococcus	unknown	149	32
		86	xanthus			
109	1444	gi72483	Homo sapiens	adaptor	1615	97
	ļ	81		protein	\	
		1		p130Cas	l	
110	1447	Y65168	Homo sapiens	Human 5' EST	403	97
			_	related		
	!	1	· ·	polypeptide ·	[ĺ
111	1457	W19919	Homo sapiens	Human Ksr-1	227	77
				(kinase	Ĺ	
				suppressor of	1	
Ĭ	j]		Ras).	ļ]
112	1471	G02532	Homo sapiens	Human	97	59
112	13/1	G02552	nomo bapieno	secreted		
ļ				protein,	ļ	
113	1473	gi60628	Homo sapiens	candidate	581	100
113	14/3	74	NOMO Saprems	tumor	502]
1		/4		suppressor]
· ·				protein DICEL		
	1 484	754006	Ware appliant	Human 5' EST	197	100
114	1474	Y64896	Homo sapiens	related	13,	100
	1					
		1		polypeptide KIAA0037	295	76
115	1483	gi43621	Homo sapiens	KIAAUU3/	295	/6
		8			133	64
116	1486	gi58528	Homo sapiens	bridging	133	04
		34		integrator-2		
117	149	gi33271	Homo sapiens	KIAA0674	2243	98
İ		62		protein		
118	1503	gi17367	Escherichia	•	1270	97
L		85	coli			
119	1506	gi40622	Escherichia	YhhI protein	612	90
1		98	coli			
120	1513	gi40623	Escherichia	•	556	94
1		46	coli			
121	1514	gi21660	Escherichia	PhoQ protein	661	90
		9	coli	1		
122	1523	gi57127	Rattus	calcium	1178	90
	1	56	norvegicus	transporter		}
				CaT1		
123	1527	gi18539	Mus musculus	glucocorticoid	171	84
123		80		receptor		
1				interacting	1	
				protein 1		
124	1536	¥17227	Homo sapiens	Human	452	100
124	1230	11/22/	TOWO BADIETTS	secreted		
I	Ī	1	<u></u>	Becreted	<u> </u>	J

<u> </u>	SEO	Acces-	Species	Description	Smith	8
SEQ ID	ID	sion	Species	Description	_	Identity
NO:	NO:	No.			Water	
1.0.	in				man	
	USSN				Score	
	09/48					
	8,725					
-				protein (clone		
				ya1-1).		
125	154	gi85150	Pinus taeda	putative	81	40
	}	90		arabinogalacta		
			Communication of the Communica	n protein Similarity to	134	34
126	1544	gi38799	Caenorhabditi	Xenopus F-	134	34
		33	s elegans	spondin	\	
				precursor (PIR		
i				Acc. No.		
i	ł	1		comes from	İ	
		1		this gene		
127	1554	gi65238	Homo sapiens	S1R protein	255	84
		17	_			
128	1555	gi66352	Homo sapiens	beta-	210	90
	ļ	05		ureidopropiona		
				se	<u> </u>	
129	1556	Y39286	Homo sapiens	Phosphodiester	161	61
ĺ		1		ase 10 (PDE10)		ĺ
		<u> </u>		clone FB93a.		
130	1564	gi89779	Streptomyces	putative	231	45
· ·		45	coelicolor	secreted serine		ŀ
1			A3 (2)	protease		
131	1576	gi30258	Rattus	signal	183	97
131	1370	28	norvegicus	transducer and		
	}	-		activator of		1
İ				transcription		
[ļ	1		4	[1
132	1578	gi51065	Homo sapiens	transcriptiona	758	98
	ļ	72		l activator	1	
İ				SRCAP		
133	1579	gi85755	Homo sapiens	toll-like	595	99
		27		receptor 8	 	
134	158	_	Mus musculus	protein kinase	168	70
	1500	8	Gallus gallus	c-Rmil	231	90
135	1580	gi63340	Homo sapiens	PKU-alpha	127	92
136	1588	gi22179 31	nouno sabrens	2.00-alpha	""	
137	1589	gi12724	Mus musculus	Phosphoinositi	720	99
13,	1337	22		de 3-kinase		
138	159	gi22246	Homo sapiens	KIAA0344	215	43
		29				
139	1600	gi10160	Rattus	neural cell	543	93
1		12	norvegicus	adhesion		
				protein BIG-2]
				precursor		
140	161	gi66495	Homo sapiens	kidney and	1651	98
		83	<u> </u>	liver proline	<u> </u>	L

SEQ	SEO	Acces-	Species	Description	Smith	
ID	ID	sion	opecies	Description	_	Identity
NO:	NO:	No.			Water	
	in				man	
ł	USSN	ļ			Score	
	09/48					
	8,725					
				oxidase 1		
141	1612	gi40611	Rattus	protein kinase	125	89
		3	norvegicus	I		
142	1615	gi21999 2	Homo sapiens	phSR2	150	78
143	1620	gi57146	Homo sapiens	serine/threo-	126	71
1	ļ	36		nine protein		
	1			kinase Kp78	,	
ļ		İ		splice variant		
	3644	177.33.50	77	CTAK75a	2542	100
144	1644	Y13352	Homo sapiens	Amino acid sequence of	2542	100
		1		protein		
ł	ł			PRO228.	/	1
145	1647	Y99444	Homo sapiens	Human PRO1575	704	100
				(UNQ781) amino	1	
ł				acid sequence		
146	1650	gi37897	Homo sapiens	transmembrane	271	100
		65	_	receptor UNC5C	Ì	
147	1663	W75258	Homo sapiens	Fragment of	163	-96
				human secreted	[
1.		<u> </u>		protein		ĺ
`				encoded by		
L				gene 26.		
148	1665	gi10432 431	Homo sapiens	secreted modular	1428	99
1		431		calcium-		
				binding		}
•		1		protein		
149	1671	gi67081	Mus musculus	inositol	169	97
		69		phosphatase		
				eSHIPD183		[
150	1672	Y68773	Homo sapiens	Amino acid	1030	99
				sequence of a	,	
				human	}	
1	1	l		phosphorylatio	<u> </u>	
				n effector	Ī	
L	1650			PHSP-5.	133	86
151	1678	gi60630 17	Homo sapiens	tousled-like kinase 1	132	,
152	1680	gi35106	Homo sapiens	nuclear	278	80
		03		receptor co-		
i		1		repressor N-		
1	1.500		Vana assiss	CoR	105	100
153	1692	gi15460 84	Homo sapiens	farnesol receptor HRR-1	165	100
154	1698	gi52046	Oryctolagus	597 aa	177	94
124	1030	9152046	cuniculus	protein	*′′	
1		1		related to		
L	L	L	<u> </u>		L	

 	CEO	Acces-	Species	Description	Smith	<u> </u>
SEQ	SEQ ID	sion	Species	Description	_	Identity
ID	NO:	No.			Water	
NO:		NO.			man	
	in				Score	1
	USSN				1 50020	
	09/48					1
	8,725			No /olugogo		
				Na/glucose		
				cotransporters		95
155	1702	gi10432 382	Homo sapiens		519	
156	1704	Y91668	Homo sapiens	Human	214	75
				secreted		
				protein		1
				sequence	,	
				encoded by	1	
İ				gene 73	ŀ]
157	1708	gi30807	Mus musculus	growth factor	457	78
		57	•	independence-	•	
				1B		
158	1716	gi29653	Homo sapiens	putative	220	92
130	1,10	9123033	1.0	oncogene	ļ	
159	173	gi34524	Rattus	serine/threo-	699	100
123	1/3	73	norvegicus	nine protein		
		/3	HOLVEGICUS	kinase TAO1]
		Y27581	Ware carions	Human	774	100
160	1731	127581	Homo sapiens	secreted	/ / -	100
1					1	
1	ļ			protein	1	}
	ĺ			encoded by		
				gene No. 15.		
161	1732	gi96520	Homo sapiens	scavenger	1025	98
	ļ	87	Ì	receptor		
	1	1		cysteine-rich	ł	1
	ļ			type 1 protein	1	
1	ŀ	i	İ	M160	1	
	ļ	1	İ	precursor		
162	174	Y35923	Homo sapiens	Extended	1691	100
ł	1	!		human secreted	1	
		ì		protein		
!				sequence,]	
163	1740	Y53014	Homo sapiens	Human	337	60
			_	secreted]
1.				protein clone		
				fn189_13		
				protein		
		1		sequence		1
164	1748	gi77702	Homo sapiens	PRO2822	218	93
1 20-4	1/20	37				}
1-25-	1751	gi89798	Homo sapiens		306	50
165	1,21	25	TOWO DAPTETTS			
1	1966	R95332	Homo sapiens	Tumor	1184	62
166	1755	K95332	TOWO Sabrens	necrosis		""
]				1	}	1
Ì				factor		
1				receptor 1		'
1		1		death domain		
1	1	1	1	ligand (clone	1	

SEQ	SEO	Acces-	Species	Description	Smith	8
ID	ID	sion	Species	Descripcion	-	Identity
NO:	NO:	No.			Water	-
	in				man	
	USSN	1			Score	
	09/48					
	8,725]				
				3TW).	1545	
167	1762	gi73809	Homo sapiens	Gem-	1545	99
		47		interacting protein		
168	1776	gi59122	Homo sapiens	hypothetical	224	100
108	1//6	65	nomo saprems	protein		-00
169	1777	Y70461	Homo sapiens	Human	413	95
1 200	1	1,0101	nome barpeoins	membrane	\	
		1		channel		1
			į	protein-11		
				(MECHP-11).]	
170	1781	R26060	Homo sapiens	Growth Factor	398	98
				Receptor Bound		
		1		protein GRB-		1
				1.		
171	1796	gi10312	Homo sapiens	serine	1381	99
		169		carboxypepti-		
				precursor		
				protein		
172	180	gi30025	Homo sapiens	neuronal	477	61
1/2	100	27	Homo Suprem	thread protein		
		1 -		AD7c-NTP	1	
173	182	gi73851	Homo sapiens	HBV pX	2066	82
		31		associated		
	Í			protein-8;		
	1			XAP-8		
174	1820	G03249	Homo sapiens	Human	370	97
		1	·	secreted		[
	1	-245225	0	protein,	1048	90
175	1822	gi47396 9	Oryctolagus cuniculus	members of	1040	'0
1	1	, ,	Cuntentus	sodium-glucose	•	} '
				cotransporter		1
		1		family		
176	1829	gi10440	Homo sapiens	FLJ00012	310	96
		355]	protein		<u> </u>
177	1832	gi16565	Oryctolagus	phosphorylase	146	96
		0	cuniculus	kinase beta-		
				subunit		
178	1834	W75132	Homo sapiens	Human	423	47
:				secreted	}	
	İ		1	protein		
1				encoded by gene 11 clone		
1		1		HCENJ40.	1	
770	1837	gi60369	Saimiriine	ORF	615	71
179	103/	9100309	herpesvirus 2	48~EDLF5~sim.		
		1		to EBV BRRF2		1
			<u> </u>	1	ــــــــــــــــــــــــــــــــــــــ	

SEQ	SEQ	Acces-	Species	Description	Smith	8
ID	ID	sion	ppccaco	2000000	-	Identity
NO:	NO:	No.			Water	-
	in				man	
	USSN				Score	,
	09/48	ļ				
1	8,725	ļ]	
180	1859	gi99896	Homo sapiens	ROR2 protein	645	87
		96				
181	1880	gi73408	Mus musculus	chondroItin	275	40
,	}	47		4-	ł	ŀ
İ		ļ	;	sulfotransfera		1
				se		
182	1881	gi75732	Homo sapiens		298	100
		91				
183	1890	gi31499	Homo sapiens	ST1C2	183	94
		50			- 542	
184	1899	gi21432	Homo sapiens	Phosphoino-	346	98
		60		sitide 3- kinase		
			· · · · · · · · · · · · · · · · · · ·	U2AF1-RS2	224	46
185	19	gi18085	Homo sapiens	UZAFI-KSZ	224	*
100	192	82 G03192	Homo sapiens	Human	267	86
186	192	G03192	HOURS Sabiens	secreted	207	
1		ļ.		protein,	.	1
187	1922	gi48585	Mus musculus	IB3/5-	1206	78
187	1922	8	Mus musculus	polypeptide		
188	1945	gi37261	Homo sapiens	porypoporac	1402	97
189	195	W67863	Homo sapiens	Human	551	98
185	1 - 2 - 3	10,000	nomo bapiono	secreted		
				protein	ł	
		[encoded by		
l	1	1	1	gene 57 clone	[
	İ			HFEBF41.	1	
190	1957	gi40673	Homo sapiens	Shb	263	44
1	}	8	1			
191	1969	Y41701	Homo sapiens	Human PRO708	975	98
				protein		
L		<u> </u>		sequence.		
192	1970	gi39798	Caenorhabditi	Weak	254	49
1	İ	17	s elegans	similarity to	1	
				Human		
		1	1	tyrosine-		
			}	protein kinase		
	<u> </u>	060555	******	CSK	365	98
193	1973	G00796	Homo sapiens	Human secreted	303	30
		1		protein,		1
122	1005	- 4550C	Homo sapiens	Putative	1420	99
194	1985	gi45586	nomo sapiens	homolog of	1420	
		37		hypoxia		
		1	1	inducible		1
Í	1			factor three		
}		1		alpha		
195	1986	gi44550	Homo sapiens	host cell	367	50
195	1,00	15		factor homolog	1	
L	1		<u> </u>	1		

CEO I	SEQ	Acces-	Species	Description	Smith	ક
SEQ ID	ID	sion	550200		_	Identity
NO:	NO:	No.			Water	
.,0.	in	3.0.			man	
	USSN				Score	
	09/48	·				
	8,725				,	
	0,723			LCP		
196	2	G02532	Homo sapiens	Human	106	85
				secreted		
				protein,		
197	2004	gi10503	Homo sapiens	type A	961	100
		935		calpain-like		
				protease	<u> </u>	
198	2023	gi16513	Escherichia	•	1075	97
	1	41	coli			
199	2025	Y71069	Homo sapiens	Human	540	100
				membrane		
	[[transport		}
]]		protein,	1	1
				MTRP-14.		
200	2038	gi85725	Homo sapiens	membrane-	686	98
	1	43		associated	Ì	1
				lectin type-C		
201	2041	gi37400	Homo sapiens	trk-2h	228	89
				polypeptide	<u> </u>	
202	2043	W75096	Homo sapiens	Human	290	38
	1			secreted		ļ
	ļ			protein	1	i
				encoded by	ŀ	
		ļ	ļ	gene 40 clone		
				HNEDJ57.	595	97
203	2068	G03394	Homo sapiens	Human	333	1 3'
				secreted		
				protein,	1025	85
204	2072	gi21165	Rattus	amino acid	1023	"
	1	52	norvegicus	transporter 3	1	
	<u> </u>	1.5546			369	39
205	2076	gi15740	Drosophila melanogaster	fat protein	305	
055	2070	9 gi10549	Gallus gallus	csH-PTP2	605	94
206	2078	g110549 40	Garrus garrus	COMPETER		
207	2004	gi96631	Homo sapiens	hypothetical	874	99
207	2084	28	Lomo Dapieno	protein		
208	2088	gi10567	Homo sapiens	sodium	609	100
208	2000	590		bicarbonate		•
		390		cotransporter-		1
				like protein		
209	2089	gi17890	Escherichia	putative ATP-	961	98
203	2009	01	coli	binding		
		"-		component of a		
				transport		
				system		1
	2097	Y70460	Homo sapiens	Human	258	96
7) 7 / 1	(202/	1 -, 0-200			1	i
210	1 .	l .		membrane		i

SEO	SEO	Acces-	Species	Description	Smith	<u> </u>
ID	ID	sion	Species	Description	-	Identity
NO:	NO:	No.			Water	
	in	""			man	
	USSN	i l			Score	
	09/48				ļ	
	8,725	}	1	j		
		-		protein-10		
			•	(MECHP-10).		
211	2108	gi32075	Rattus	hexokinase	767	74
		08	norvegicus			
212	2111	gi63302	Homo sapiens	KIAA1176	3710	99
		33		protein		
213	2118	W74797	Homo sapiens	Human	156	96
				secreted		1
				protein		
		ļ		encoded by		
	į			gene 68 clone		
214	2134	gi17809	Homo sapiens	branched	209	97
214	2134	91	nomo saprens	chain acyl-CoA	203	
	ļ	}		oxidase		
215	2146	gi76881	Homo sapiens	hypothetical	1038	100
213	2140	48	nomo papadia	protein		
216	2149	gi22804	Homo sapiens	KIAA0376	917	100
		85	•			1
217	2153	gi18424	Rattus	ankyrin	592	88
1	1	29	norvegicus	binding cell		
	ļ			adhesion		1
	Ì			molecule	1	
				neurofascin		
218	2155	gi65267	Homo sapiens	Eps15R	1126	100
		91		000000		33
219	2161	gi73004	Drosophila	CG7709 gene	200	33
		27 Y52296	melanogaster	product	186	91
220	2163	Y52296	Homo sapiens	isomerase	100	31
l			Í	homologue-3	ì	
		1		(HIH-3).		
221	2173	W34526	Homo sapiens	hTCP protein	164	93
221	21/3			fragment.		
222	2178	gi33605	Rattus	Citron-K	299	94
] ·]	12	norvegicus	kinase	1	
223	2180	Y74008	Homo sapiens	Human	261	41
1			_	prostate tumor		
ļ		1		EST fragment		
				derived		
				protein #195.		<u></u>
224	2184	gi53041	Mus musculus		130	41
225	2186	gi40177	Homo sapiens	ribosomal	142	64
		4		protein S6		
		<u> </u>		kinase 3	 	ļ
226	2190	gi57729	Homo sapiens	The hal225	176	100
		5		gene product		
ł	1	1		is related to		
	1	<u> </u>	<u> </u>	human alpha-	<u> </u>	<u> </u>

SEQ	SEQ	Acces-	Species	Description	Smith	8
ID	ID	sion	Species	200011	_	Identity
NO:	NO:	No.			Water	-
NO:	in	no.	1		man -	
	USSN				Score	
	09/48	,	l	4		ļ
	8,725					
	0,723			glucosidase.		
227	2210	gi20553	Rattus	transmembrane	620	90
22,		92	norvegicus	receptor		
				UNC5H1	•	
228	2214	gi78617	Homo sapiens	low density	1360	98
		33	_	lipoprotein	· ·	
				receptor		
				related	`	
				protein-	1	
	İ		,	deleted in	ļ	
	ĺ	(tumor	[
229	2223	qi79591	Homo sapiens	KIAA1464	884	99
		89	•	protein		
230	223	W88627	Homo sapiens	Secreted	300	77
250			-	protein		
	i	1		encoded by		
	ļ			gene 94 clone		
				HPMBQ32.)	
231	2233	gi78395	Homo sapiens	organic anion	1092	99
231	2233	87		transporting		
	ļ			polypeptide 14	1	
232	2237	gi10440	Homo sapiens	FLJ00033	1212	99
232	223,	400		protein	1	
233	2251	gi59237	Homo sapiens	zinc metallo-	277	44
233	2231	86	110	protease		
		""	•	ADAMTS6	1	1
234	2256	W63698	Homo sapiens	Human secreted	516	100
23.			•	protein 18.		
235	2259	gi46787	Homo sapiens	hypothetical	387	36
233		22	•	protein		
236	2262	Y33741	Homo sapiens	Beta-	793	99
250		1]	secretase.		
237	2265	gi70185	Homo sapiens	hypothetical	608	94
""		45		protein		
.238	2271	gi41861	Homo sapiens	unknown	684	53
.236		83		1		
239	2273	gi72430	Homo sapiens	KIAA1327	1031	100
239	"","	35		protein		
240	2280	gi58096	Homo sapiens	sperm membrane	342	95
240	2200	78		protein BS-63		
241	2286	gi62246	Homo sapiens	Na+/sulfate	1221	99
1 271	""	91		cotransporter		1
	1			SUT-1	1	
242	2291	gi20762	Rattus	uromodulin	345	50
	~~~	1	norvegicus			
243	2292	gi72963	Drosophila	CG5274 gene	272	35
243	22,52	04	melanogaster	product		
244	2294	Y28503	Homo sapiens	HGFH3 Human	320	98
244	2274	120303	110 Dapteris	Growth Factor		
L		<u> </u>	<u> </u>	1	·	

SEQ	SEQ	Acces-	Species	Description	Smith	8
ID	ID	sion	Specics	Description	-	Identity
NO:	NO:	No.			Water	
110.	in	1.0.			man	
	USSN			-	Score	1
	09/48	i l				
	8,725	l				
	0,123		<u> </u>	Homologue 3.		
245	2296	W88799	Homo sapiens	Polypeptide	223	86
			_	fragment		
		'		encoded by		
	l			gene 45.		
246	2303	gi71101	Homo sapiens	guanine	1212	99
		60		nucleotide		
				exchange	\ \ \	
				factor	ļ	,
247	2306	gi64348	Mus musculus	calcium/calmod	576	84
		74		ulin dependent	[	
1	]	1		protein kinase	]	]
{	[			kinase alpha		
248	2309	Y95433	Homo sapiens	Human calcium	1203	99
			_	channel SOC-	1	į
				2/CRAC-1 C-	}	i i
i	i	l i		terminal	1	1
ļ				polypeptide.		
249	2313	gi73009	Drosophila	CG4677 gene	689	79
		43	melanogaster	product	İ	ii
250	2318	W48351	Homo sapiens	Human breast	202	59
				cancer related	}	
İ	-			protein		1
ļ				BCRB2.		
251	2329	G01772	Homo sapiens	Human	311	84
	ŀ			secreted		
	<u></u>	ļ		protein,		
252	2330	Y41729	Homo sapiens	Human PRO1071	886	99
1				protein		
				sequence.	268	1 12
253	2342	gi37864	Caenorhabditi	1	268	42
	L	30	s elegans	protoin	571	79
254	2350	gi93010	Homo sapiens	protein- tyrosine	5/1	'5
1		4		phosphatase		1
L	1 2350		Homo sapiens	CC chemokine	679	99
255	2359	gi93925	HOMO Saprens	CCL28	""	'
125	12261	91 gil6666	Mus musculus	alpha-NAC,	357	41
256	2361	89	Mas mascaras	muscle-	33.	
		07	1	specific form	1	1
		1		gp220	1	
257	2374	G03172	Homo sapiens	Human	112	78
23'	43/4	0031/2	TOWN DAPTETTS	secreted		
1				protein,		
258	2387	gi13991	Homo sapiens	pyruvate	201	85
238	230/	97	Lomo Dapteris	dehydrogenase		
		''		kinase isoform		1
,				4	]	
259	2401	G01757	Homo sapiens	Human	612	99
ودع		1 002/07		1	<u> </u>	1

SEQ SEQ Acces- Species Description Smith ID ID sion NO: NO: NO. Water in USSN 09/48 8,725  Secreted protein,  260 2409 gil8112 Homo sapiens cleavage signal 1 protein	% Identity
NO: NO: NO. Water man Score 9/48 8,725 secreted protein, 260 2409 gil8112 Homo sapiens cleavage signal 1	
in USSN 09/48 8,725 secreted protein,  260 2409 gil8112 Homo sapiens cleavage signal 1	86
USSN 09/48 8,725 Score  8 secreted protein,  260 2409 gil8112 Homo sapiens cleavage signal 1	86
09/48 8,725 secreted protein, 260 2409 gil8112 Homo sapiens cleavage signal 1	86
8,725 secreted protein,  260 2409 gil8112 Homo sapiens cleavage signal 1	86
secreted protein,  260 2409 gil8112 Homo sapiens cleavage signal 1	86
260 2409 gi18112 Homo sapiens cleavage 194 signal 1	86
3 signal 1	86
1 1 1 1 1 1 1 T	1 "
	}
1	
261 2431 gi70185 Homo sapiens hypothetical 473	50
47 protein	
262 2432 gi48264 Homo sapiens 327	39
96   96   100   96   100   96   100   96   96   96   96   96   96   96	97
263 2467 G03667 Homo sapiens Human 640 secreted	''
protein,	j
	91
264 2471 gi76881 Homo sapiens hypothetical 1284	
265 2478 gi79081 Homo sapiens polycystic 615	90
265 2476 9175001 nome supreme portrolled kidney	
disease-	
associated	
protein	
266 2484 gi33270 Homo sapiens KIAA0633 1747	99
80 protein	!
267 249 G03793 Homo sapiens Human 139	65
secreted	
protein,	
268 2490 gi64673 Homo sapiens thyrotropin- 757	98
71 releasing	
hormone	
degrading	
ectoenzyme  269 25 G03203 Homo sapiens Human 137	65
269 25 G03203 Homo sapiens Human 137	65
protein,	]
	74
270 2504 gi40977 Homo sapiens HBV 166	
factor	
271 2506 gi20727 Homo sapiens Na+/nucleoside 201	95
84 cotransporter	
272 2507 gi59240 Homo sapiens 335	38
07	•
273 2510 gi77173 Homo sapiens beta-site 383	89
85 APP-cleaving	
enzyme 2, EC	
3.4.23.	
274 2523 gi33970 Homo sapiens 150	96
275 253 gi36615 Homo sapiens serine/threo- 391	77
nine protein	
kinase	
276 2533 gi45896 Homo sapiens KIAA0985 191	61

SEQ	SEQ	Acces-	Species'	Description	Smith	ક
ID	ID	sion	DP00101	# 0000 P		Identity
NO:	NO:	No.			Water	_ }
	in				man	
	USSN				Score	;
	09/48	}			•	
	8,725					
		14		protein		
277	2536	gi20886	Caenorhabditi	strong	419	55
	ļ	85	s elegans	similarity to		
		1	•	the CDC2/CDX	ļ	
	•			subfamily of	1	}
				ser/thr		
				protein kinases	\	
	2544		Mus musculus	YSPL-1 form 2	280	80
278	2544	gi10024 25	Mus musculus			
279	2568	Y41738	Homo sapiens	Human PRO541	379	49
	]	}		protein	}	
<u></u>				sequence.		
280	2580	gi30044	Rattus	putative	382	49
		82	norvegicus	integral		
İ				membrane		l i
				transport		
		10000		protein	582	50
281	2593	gi73000	Drosophila melanogaster	CG4525 gene product	362	50
	2600	49 gi45304	Homo sapiens	thyroid	334	90
282	2600	37	HOMO SAPIENS	hormone	33*	'
· ·		3'		receptor-		
				associated		]
1				protein		
				complex		
				component		
1		1		TRAP240		
283	2625	gi80996	Homo sapiens	toll-like	761	96
		52		receptor 9		
	}			form A		
284	2641	gi14801 9	Escherichia coli	tolA	692	100
285	2667	gi17503	Pseudomonas	Carbamoy1-	143	76
		87	aeruginosa	phosphate	ľ	
1.			_	synthetase		]
l	1	}		large subunit	<u> </u>	
286	2670	gi48834	Mus musculus	RNA binding	139	92
		37		protein	<u> </u>	
287	2673	Y66656	Homo sapiens	Membrane-	1869	98
1	1	1		bound protein	1	
			<u> </u>	PRO943.	<del> </del> _	
288	2676	gi38859	Mus musculus	mismatch-	123	88
1	İ	78		specific		
1		1		thymine-DNA		
		-261532	Home geniene	glycosylate hypothetical	465	82
289	2680	gi64534 38	Homo sapiens	protein	703	02
1 200	2002	gi18417	Mus musculus	GATA-5	527	77
290	2682	911841/	I mus muscurus	J GRIA J	1 32.	<u> </u>

SEQ	SEQ	Acces-	Species	Description	Smith	*
ID	ID	sion	opecies	Debotapone	-	Identity
NO:	NO:	No.			Water	1
NO:	in	1.0.			man	
	USSN				Score	[
,	09/48				00010	
	8,725	56		cardiac		
		36		transcription		
}		ļ		factor		
	3504	-÷09449	Homo sapiens	nicotinic	294	88
291	2684	gi98449 20	HOMO Saprens	acetylcholine	254	00
ļ	1	20		receptor	ļ	
ļ	ŀ	ļ		subunit alpha		
l	1	Ì		10	\ \	1
<u> </u>		1	Nachaniahia		879	98
292	2695	gi17897	Escherichia	putative	0/9	1 30 1
		64	coli	transport	036	00
293	2697	gi34922	Escherichia	peripheral	936	99
	1	9	coli	membrane	]	]
				protein		
294	2698	gi40621	Escherichia	•	737	100
		94	coli	·		
295	2700	gi52924	Escherichia	homoserine	578	100
	ļ	0	coli	kinase	<u> </u>	
296	2704	gi15528	Escherichia	hypothetical	420	100
	1	31	coli		L	
297	2712	gi17896	Escherichia	putative ATP-	262	100
1		72	coli	binding		
				component of a	ŀ	1
	İ			transport		
		1		system		
298	2716	gi40624	Escherichia	Transmembrane	382	100
1	1	09	coli	protein dppC	l	
299	2719	gi30497	Escherichia	matches	921	95
		6	coli	PS00017:	1	Į į
	i			ATP_GTP_A and	J	]
	1	1		PS00301:	1	
	ì	1	1	EFACTOR_GTP;	1	
				similar	1	
300	2724	gi14585	Escherichia	nmpC	647	97
		6	coli			
301	2725	gi17894	Escherichia	putative	312	100
		73	coli	transport		]
1		1		protein		
302	2728	gi18055	Escherichia		222	97
		61	coli	,		
303	2729	gi43248	Escherichia		655	91
			coli			
304	2744	gi39629	Escherichia	similar to E.	675	100
1 332	-,	9	coli	coli pyruvate		}
				formate-lyase		
1				activating	1	
		1		enzyme		
305	2749	gi17426	Escherichia	<del>                                     </del>	592	100
1 303	"'"	48	coli			
306	2752	gi40622	Escherichia	Sensor kinase	357	100
300	2/52	9120022	1			

SEQ	SEO	Acces-	Species	Description	Smith	- 8
ID	ID	sion	phecres	Description	-	Identity
NO:	NO:	No.			Water	
NO.	in				man	}
	USSN				Score	
	09/48	[ 1			!	'
	8,725	1				
		36	coli	CitA		
307	2762	gi17877	Escherichia	putative	342	100
		95	coli	LACI-type		
ĺ	İ			transcriptiona	i	
				l regulator		
308	2764	gi17997	Escherichia	putative	151	84
		43	coli	LACI-type		1
				transcriptiona	,	
		}		1 regulator		]
309	2768	gi40596	Escherichia	yohG	534	94
		4	coli			
310	2774	gi40623	Escherichia	•	387	97
		38	coli			
311	2790	gi40623	Escherichia	•	420	86
		38	coli			
312	2800	gi17898	Escherichia	putative	572	100
L		05	coli	transport	100	40
313	2811	gi53053	Mus musculus	protein	421	49
L	<u></u>	33		kinase Myak-S		97
314	2827	gi10047	Homo sapiens	KIAA1588	531	97
		251		protein.	185	62
31.5	2830	G02872	Homo sapiens	Human secreted	185	62
1				protein,	i	
	2036		Cricetulus	cAMP-	1677	97
316	2836	gi19117	sp.	dependent	10,,	]
1			ap.	protein kinase	1	
				alpha-	1	
Ì				catalytic	ł	
ļ		1		subunit		
317	2851	gi55884	Homo sapiens	BCL2/adeno-	220	61
1		6		virus E1B		
-	1	1		19kD-	1	
1		1		interacting		
		1		protein 3		
318	2856	gi38822	Homo sapiens	KIAA0745	232	93
1		11		protein		_
319	2866	gi63297	Homo sapiens	KIAA1119	1331	91
		08		protein	<u></u>	<u> </u>
320	2874	gi28530	Mus musculus	tousled-like	203	82
1		33		kinase		
321	2882	gi10185	Schizosacchar	hypothetical	318	42 -
{		134	omyces pombe	zinc-finger		Į.
				protein		
322	2886	G03797	Homo sapiens	Human	140	69
1		}		secreted		
				protein,	<del>                                     </del>	ļ <u></u> -
323	2899	gi42403	Homo sapiens	KIAA0918	170	53
L		25	I	protein	<u></u>	<u> </u>

		<del></del>			Smith	8
SEQ	SEQ	Acces- sion	Species	Description	Smith	Identity
ID NO:	ID NO:	No.	ļ		Water	Identity
140:	in	NO.			man	
	USSN				Score	
	09/48	~′				
	8,725					
324	2906	Y94988	Homo sapiens	Human	1738	100
				secreted		
				protein vl1_1,		
325	2920	gi94537 35	Homo sapiens		1926	100
326	2925	gi64348	Homo sapiens	CDK4-binding	1210	100
		76		protein		
			•	p34SEI1		
327	2930	gi39413	Schistosoma	myosin	208	28
		20	japonicum			
328	2934	Y31645	Homo sapiens	Human	642	63
	İ	1		transport- associated	[	
				protein-7 (TRANP-7).		
329	2955	G01165	Homo sapiens	Human	528	99
329	2933	GUITES	nouto sapiens	secreted	320	
				protein,		
330	2967	gi72639	Homo sapiens		466	100
		60				
331	2980	gi45895	Homo sapiens	KIAA0943	1849	94
		30		protein		
332	2994	G03812	Homo sapiens	Human	124	61
				secreted		
			******	protein,	2666	98
333	2996	gi98574 00	Homo sapiens	endothelial	2000	36
	•	00		marker 1		
				precursor	1	
334	2999	¥66697	Homo sapiens	Membrane-	2254	100
				bound protein	1	
1		1		PRO1383.		
335	3	gi62890 72	Homo sapiens	JM24 protein	930	100
336	3008	Y45219	Homo sapiens	Human CASB47 protein.	557	92
337	3013	gi52626	Homo sapiens	hypothetical	1747	100
		78	_	protein	ĺ	l
338	3041	Y73335	Homo sapiens	HTRM clone	1315	99
	ł	1		1850120 protein	1	1
				sequence.	1	
339	306	gi48684	Mesocricetus	Mx-	1867	95
339	308	43	auratus	interacting		1
	1	1		protein kinase	1	1
		1		PKM		
340	3061	gi43333	Homo sapiens	protein-	3934	94
		8		tyrosine	1	1
				kinase		1

and.	770	3	- Consider	Description	Smith	
SEQ	SEQ	Acces- sion	Species	peacription	SILLCII	Identity
ID NO:	ID NO:	No.			Water	Identity.
NO:	in	NO.	•		man	-
	USSN	1	1		Score	
	09/48				55525	
	8,725				ł	
341	309	Y76145	Homo sapiens	Human	1313	99
				secreted		
				protein		
				encoded by		
				gene 22.		
342	3095	gi73001	Drosophila	CG14899 gene	190	57
		59	melanogaster	product		
343	3098	gi53205	Homo sapiens	protein-	2641	86
		6		tyrosine-		Ì
				phosphatase	100	
344	3105	gi28598	Homo sapiens	mitochondrial	192	71
		7		outer membrane protein 19	1	·
245	3333		Macaca		180	61
345	3118	gi99299	Macaca fascicularis	hypothetical protein	180	0.7
346	3124	35 gi81319	Mus musculus	transient	226	100
346	3124	03	Mus musculus	receptor	220	100
		03		potential-		
				related		
		1		protein	1	
347	3126	Y02370	Homo sapiens	Polypeptide	261	100
			,	identified by	ļ	
	Ì	}		the signal		
1	ļ	1		sequence trap		l
				method.		
348	3166	gi72908	Drosophila	CG1531 gene	534	42
		60	melanogaster	product		
349	3175	gi66495	Homo sapiens	kidney and	1752	95
		83		liver proline		ŀ
	1		******	oxidase 1	1048	OF.
350	3176	gi72084	Homo sapiens	long-chain 2-	1048	95
1		38		hydroxy acid oxidase HAOX2		
351	3188	Y02693	Homo sapiens	Human	243	57
327	3100	102093	TOWN Bapterra	secreted		"
J ·		1		protein		
				encoded by		
	1			gene 44 clone		
				HTDAD22.		
352	3191	gi71059	Homo sapiens	calcium	300	96
		26		channel		
				alpha2-delta3		1
1				subunit	<u> </u>	
353	3208	gi10334	Homo sapiens	MUCDHL-FL	613	98
		774				
354	3226	Y87209	Homo sapiens	Human	3147	99
		1	ĺ	secreted		]
				protein	1	
		L	<u></u>	sequence	<u> </u>	<u></u>

			· · · · · · · · · · · · · · · · · · ·		C-1+4	ક
SEQ	SEQ	Acces-	Species	Description	Smith	Identity
ID	ID	sion			Watan	Identity
NO:	NO:	No.			Water	
	in				man	ļ
	USSN				Score	1
	09/48				Ì	ļ
	8,725					
355	3235	gi67151	Homo sapiens	Fanconi	1947	99
		35		anemia,	ľ	
		Į.	i	complementatio		
				n group F		
356	3257	gi54416	Canis	zinc finger	326	42
	İ	15	familiaris	protein		
357	3282	G03002	Homo sapiens	Human	211	61
			•	secreted	· `	
				protein,		
358	3289	gi32884	Homo sapiens	PI3-kinase	5832	97
	<b>[</b>	57				
359	3296	gi77701	Homo sapiens	PRO1722	293	64
		39	_		j	ļ
360	3298	gi21988	Ambystoma	electrogenic	1278	52
	5-2-5	15	tigrinum	Na+		
	-		<b>J</b>	bicarbonate		
l	i			cotransporter;	1	
1				NBC	ł	1
361	3303	gi40280	Homo sapiens	potassium	1881	92
1 301	3303	15		channel	1	1
362	3305	gi59029	Homo sapiens	very large G-	1770	100
302	3303	66	nomo bapieno	protein	}	
		00		coupled	ł	
				receptor-1	1	
363	3308	gi21994	Homo sapiens	The first in-	3967	86
303	3300	4	nomo suprems	frame ATG	1	
1		-		codon is		
	ł			located at	}	
}	j	į		nucleotides	1	}
				NPPase.	ļ	
764	3325	gi35102	Homo sapiens	R31237 1,	192	94
364	3345	34	TOUG Saprens	partial CDS		
7.55	3341	W78899	Homo sapiens	Human UNC-5	1614	90
365	3341	7/0033	TOWO Sabrens	homologue	-51-	-
		1	]	UNC5H-1.		
1-355	3343	mi14700	Mug muggulus	PNG protein	341	70
366	3342	gi14782	Mus musculus	I swg brocern	] 341	
	<del> </del>	05	D	mornilates of	2263	98
367	3350	gi27394	Bos taurus	regulator of	2203	J 98
		60	1	G-protein		
		<del></del>	L	signaling 7	1 3 ==	79
368	3372	gi76716	Homo sapiens		375	/9
		63		ļ	1-0555	122
369	338	Y84322	Homo sapiens	A human	2606	100
		1	1	cardiovascular		1
				system		
				associated		
				protein		
		1		kinase-3.		<u> </u>
370	3383	gi10441	Homo sapiens	protein	1127	100
	.1		·			

	050			Danamiation	Smith	
SEQ ID	SEQ ID	Acces- sion	Species	Description	Smith	Identity
NO:	NO:	No.			Water	ruencicy
140.	in	1.0.			man	
	USSN			•	Score	
	09/48					
	8,725	ł				
		382	· .	kinase		
371	3395	gi53082	Homo sapiens	epidermal	402	47
	i	3		growth factor		
		1		receptor kinase		
	}			substrate		
372	3405	Y29332	Homo sapiens	Human	1220	94
312	3403	123332	nomo saprens	secreted	122,5	]
				protein clone		
		,		pe584_2		
				protein	ļ	
				sequence.		
373	3408	gi33347	Homo sapiens	shal-type	2888	90
		41		potassium		
				channel		
374	345	gi45395	Homo sapiens	NAALADase L protein	600	72
375	346	Y95434	Homo sapiens	Human calcium	1802	99
3/3	340	199434	nomo sapiens	channel SOC-	1002	
				3/CRAC-2 C-		
				terminal		
				polypeptide.		
376	3470	gi97984	Homo sapiens	putative	277	100
	1	52		capacitative		
				calcium		
377	3482	gi38185	Homo sapiens	channel cAMP-specific	2353	96
3//	3402	72	your sabiens	phosphodiester	2353	36
		/-		ase 8B;		
		1		PDE8B1; 3',5'-		
ļ	1	1		cyclic	1	i .
		1		nucleotide	}	
Ì		]		phosphodiester		
				ase		
378	3492	gi16658	Homo sapiens		3878	99
379	3530	25 gi50510	Homo sapiens	KIAA0066	3637	100
3/9	3530	g150510	HOURD Sabreits	KIMMOODO	303/	
380	3533	Y32169	Homo sapiens	Human growth-	2860	99
	5555			associated		]
				protease		
				inhibitor		
				heavy chain		
				precursor.		
381	3545	gi66241 33	Homo sapiens		449	. 98
382	3549	gi14691	Homo sapiens	The KIAA0135	5374	99
		93		gene is		
				related to	1	

070	CEO	A0000-	Species	Description	Smith	*
SEQ	SEQ ID	Acces- sion	species	Description.	-	Identity
ID NO:	NO:	No.			Water	
NO:	in	NO.			man	
	USSN				Score	1
	09/48					
	8,725					
				pim-1		
				oncogene.		
383	3595	gi63301	Homo sapiens	KIAA1169	1893	100
		90		protein		
384	3601	g180891	Homo sapiens	tumor	992	99
		5		necrosis		i
	Ì	ļ		factor	\	ł
				receptor type 1 associated		[
		<u>'</u>		protein		
305	3612	gi53054	Mus musculus	SH2-B PH	1439	92
385	3014	g153054 48	MASCULUS	domain		1
	]	30		containing		ì
		[		signaling	l	i
				mediator 1	İ	
	1	İ	!	gamma isoform	1	1
386	3613	Y32194	Homo sapiens	Human	1438	100
			_	receptor		ł
	Į			molecule (REC)		ļ
-				encoded by	1	1
				Incyte clone	1	
			<u></u>	266775.		
387	3621	gi89784	Mus musculus		393	68
	ļ	9		ubiquitinating		j
				enzyme E2-230 kDa		
200	3634	R47858	Homo sapiens	Human LDL	2895	100
388	3624	R4/838	HOURD Saprens	receptor	1000	
		ļ	l .	Domains 1 and		
	İ	1	1	2.	1	
389	3625	Y57949	Homo sapiens	Human	1868	100
		}	]	transmembrane	1	
	ľ	1		protein HTMPN-	ļ	
		}		73.		
390	3626	W69342	Homo sapiens	Secreted	442	94
				protein of	1	}
				clone CJ424_9.		92
391	3627	gi65371	Homo sapiens	putative	982	32
		36	ļ	organic anion		}
		1,00000	Trama gandana	transporter	1109	91
392	3630	Y06886	Homo sapiens	polypeptide.	1109	
355	1 3642	- 100CA	Homo sapiens	hypothetical	570	52
393	3642	gi48864 67	HOUR Saprens	protein	1	]
304	3645	gi95884	Homo sapiens	P+000111	598	98
394	3043	02	1101110 Dupation			
395	3647	Y12050	Homo sapiens	Human 5' EST	517	98
				secreted		
	1	1	ì	protein	I	Ī

ano l	000	7	Species	Description	Smith	- P
SEQ ID	SEQ ID	Acces- sion	Species	Description	-	Identity
NO:	NO:	No.			Water	
NO:	in	NO.			man	
	USSN				Score	
	09/48					
	8,725			}		
396	3653	Y70018	Homo sapiens	Human	2232	99
	ļ			Protease and		
	1			associated	1	
		i	,	protein-12		
				(PPRG-12).		
397	3676	W67818	Homo sapiens	Human	338	100
		ļ		secreted	\	j
	İ			protein encoded by		
				gene 12 clone		
				HMSJJ74.		
398	3677	gi32093	Homo sapiens	HGMP07J	650	52
398	3681	Y48443	Homo sapiens	Human	803	93
333	3001	140443	LOMO DAPACIO	prostate		
				cancer-		
}				associated	l	
				protein 140.		
400	3682	gi46917	Homo sapiens	ARF GTPase-	2435	91
		26	_	activating		
1		}	ļ	protein GIT1	}	
401	3688	gi66938	Homo sapiens	ubiquitin-	1995	99
		24		specific		
		<u> </u>		protease		
402	3689	Y94927	Homo sapiens	Human	530	81.
	ŀ	İ	1	secreted		
		1		protein clone		
		1		ck213_12 protein		1
ĺ	[	1	1	sequence		
403	3690	gi18716	Oryctolagus	ryanodine	594	95
403	3030	12	cuniculus	receptor	55.	
404	3706	gi60027	Homo sapiens	membrane-type	2630	94
***	5,55	14		serine		1
}	1			protease 1	1	1
405	3714	gi26957	Homo sapiens	SPOP	553	81
	1	. 08			<u> </u>	<u> </u>
406	3720	gi93092	Homo sapiens	asc-type	566	95
1		93		amino acid		
	<u></u>			transporter 1	1	
407	3726	gi10440	Homo sapiens	FLJ00026	1023	69
		381		protein	1-242	0.5
408	373	gi57146	Mus musculus	alpha 2 delta calcium	243	95
1	}	96	1	channel	Į.	1
1			1	subunit		
400	7700	gi69112	Homo sapiens	type II	841	100
409	3788	19	HOWO Sabrens	membrane	577	200
1		1 19		serine	1	
1				protease		
			<u> </u>	1	1	<u> </u>

SEQ	SEQ	Acces-	Species	Description	Smith	*
ID	ID	sion			-	Identity
NO:	NO:	No.			Water	
	in				man	
ł	USSN	l			Score	
	09/48					
į	8,725					
410	3789	Y45023	Homo sapiens	Human sensory	1084	95
			•	transduction		
				G-protein		
				coupled	1	ĺ
			•	receptor-B3.		
411	3790	gi15240	Homo sapiens	Polio virus	1508	99
711	3,50	88	noing papaons	receptor		
				protein	\	
412	3801	gi67236	Homo sapiens	mitotic	2035	99.
412	3601	75	nomo saprens	kinase-like		
		/3		protein-1		
43.3	3803	gi96897	Homo sapiens	mitotic	332	86
413	3803	g196897	nomo saprens	kinase-like	332	"
		د		protein-1	1	!
	3000	17704	Tiene coniona	NK receptor	1988	99
414	3820	gi17704	Homo sapiens	NK receptor	1300	33
		78	77		1493	99
415	3831	gi27813	Homo sapiens	•	1493	99
		86			2243	99
416	3837	gi93678	Homo sapiens	neuronal	2243	99
		40		apoptosis		
				inhibitory	Ì	
				protein 2		
417	385	gi15269	Homo sapiens	ryanodine	149	96
		78		receptor 2	<u> </u>	
418	3856	gi99565	Homo sapiens	interleukin-	147	100
		4		11 receptor		
419	386	gi49600	Mus musculus	T2K protein	669	66
		38		kinase homolog		
420	3861	Y74129	Homo sapiens	Human	842	98
i	l			prostate tumor		1
		ļ		EST fragment		
	l			derived		
				protein #316.		
421	3883	gi66352	Homo sapiens	beta-	1576	100
1		05		ureidopropiona		
ļ				se		
422	3898	gi37231	Homo sapiens	DNA	8436	99
1	l			topoisomerasė	l	
				II		
423	3921	gi86488	Homo sapiens	putative	131	100
	1	81	_	organic anion		
				transporter	1	
424	3932	q185757	Homo sapiens	KRAB zinc	1935	99
		75		finger protein		
425	3934	gi46891	Homo sapiens	SIH003	127	92
		28				
426	3963	gi32129	Homo sapiens		339	64
		96				
<u></u>	3974	G03790	Homo sapiens	Human	232	63
427	1 33/4					

CEO.	SEQ	Acces-	Species	Description	Smith	*
SEQ ID	ID	sion	opecies	Descriptions	-	Identity
NO:	NO:	No.			Water	-
NO.	in				man	
	USSN				Score	
	09/48	1		· ·		
	8,725					}
	3,725			secreted		
				protein,		
428	3983	gi18197	Homo sapiens	vascular	433	85
•	ļ.	1		endothelial	!	
	1			growth factor		
429	3999	gi16574	Sus scrofa		484	75
		64		calcium/calmod		ę.
	1			ulin-dependent	,	
		}		protein kinase		
				II isoform	1	
				gamma-G		
430	4001	gi65722	Homo sapiens		329	100
		30				
431	4009	gi21432	Homo sapiens		521	99
		60		phosphoinositi de 3-kinase		
				de 3-kinase	1372	56
432	401	gi65723 79	Homo sapiens		13/2	30
433	4020	gi28156	Homo sapiens	tumor	1252	100
433	4020	24	nomo bapieno	necrosis		
	•	2.4	†	factor		
	1	1		superfamily	}	}
		Ì		member LIGHT		
434	4024	Y21166	Homo sapiens	Human bcl2	84	40
333				proto-oncogene		
1	1	1		mutant protein	ļ	1
ļ		1		fragment 14.		
435	4040	Y57285	Homo sapiens	Human GPCR	1726	99
		1		protein		
		1		(HGPRP)		
				sequence		1
ł	1		1	(clone ID	1	
		1		2214673).		
436	4057	W74873	Homo sapiens	Human	531	100
1		[		secreted		
		1		protein		1
1				encoded by		1
1	ł	}		gene 145		1
L		<u> </u>		clone HFXHL79.	<del> </del>	ļ <u>.</u>
437	4066	G03714	Homo sapiens	Human	92	70
	]			secreted		
		1		protein,	1077	92
438	4067	gi83317	Homo sapiens	LU1 protein	1077	34
	1-,	60	Home designs	Unman	996	100
439	4078	Y57900	Homo sapiens	Human transmembrane	356	
1		1		protein HTMPN-		}
1	1			procein Himph-		
440	4120	gi18715	Homo sapiens	mitogen-	927	100
440	1 -120	13+10,13	1 Bapacins	1		

						<del></del>
SEQ	SEQ	Acces-	Species	Description	Smith	8
ID	ID	sion			- ***	Identity
NO:	NO:	No.			Water	
	in			ł	man Score	
	USSN	•	,		SCOLE	
	09/48					
	8,725			activated		
		39		protein kinase		
				phosphatase 4	1	
	4103	gi53601	Homo sapiens	NY-REN-58	140	100
441	4123		HOMO Saprens	antigen	110	-00
4.45	4330	25 gi62890	Homo sapiens	JM24 protein	604	100
442	4130	•	Homo Sapiens	0M24 process	004	
- 443	4122	72 gi85755	Homo sapiens	toll-like	755	100
443	4133		HOMO Saprens	receptor 8	1 /33	-55
444	47.00	27 gi61185	Homo sapiens	DEAD-box	2512	100
444	4166	55	HOWO Saprens	protein .	2312	
	İ	33		abstrakt		į
445	4167	gi38008	Rattus	putative four	615	93
445	416/	30	norvegicus	repeat ion	015	
		30	nor vegicus	channel		
446	4172	gi72096	Homo sapiens	potassium	369	100
440	41/2	76	nome paparens	channel Kv8.1		
447	4185	gi53054	Homo sapiens	Na+/H+	1769	100
44/	4103	05	nome supremb	exchanger		
		05		isoform 2		ļ
448	4197	gi28111	Xenopus	NaDC-2	524	69
440	4137	22	laevis		}	1
449	4203	Q89840	Homo sapiens	Human death	198	97
***	1200	aa1		associated	1	1
Į .				protein DAP-	-	
İ	İ	Í		3.	1	
450	4262	gi59014	Marmota	olfactory	209	92
	1	78	marmota	receptor		_
451	4276	gi32456	Homo sapiens	protein-	3270	99
				tyrosine	]	
		1	Ì	phosphatase	1	·
452	4283	R41231	Homo sapiens	GAT-2	477	100
1			İ	transporter	1	
				gene.		
453	4331	gi31719	Homo sapiens	RAMP2	443	98
ļ		12				
454	4340	gi81182	Homo sapiens	unknown	1330	100
		23				
455	4351	gi17545	Rattus		2050	92
1		15	norvegicus	aminopeptidase		
		1		-B		
456	4354	Y57906	Homo sapiens	Human	1402	100
				transmembrane		
]	ļ			protein HTMPN-	}	1
1				30.		<u> </u>
457	4385	gi55964	Homo sapiens	candidate	509	97
1	1	33		tumor	1	
1	1			suppressor	1	1
				protein NOC2		

C 270	OHO.	A = = = =	Species	Description	Smith	<u>%</u>
SEQ ID	SEQ ID	Acces- sion	phecres	Description	-	Identity
NO:	NO:	No.			Water	
NO.	in				man	
	USSN				Score	j
	09/48					1
	8,725					
458	4388	W78140	Homo sapiens	Human	100	94
			_	secreted		1
				protein		
				encoded by	<u> </u>	
				gene 15 clone		
				HSDES04.		
459	4405	Y48226	Homo sapiens	Human	1246	99
				prostate		
				cancer-		
				associated	ł	
1.5	443		Bovine	protein 12.	106	35
460	441	gi29153 6	herpesvirus 1	BICP4	100	33
461	4417	gi65625	Homo sapiens	sialin	939	100
461	441/	33	nomo sapiems	5141111		
462	4419	gi18415	Homo sapiens	NG5	146	33
702	1111	55				
463	4443	gi49613	Mus musculus	AMPA	262	94
		9		selective		
1				glutamate		
				receptor	_	
464	4470	gi72483	Homo sapiens	adaptor	2592	100
		81		protein		
				p130Cas		
465	4482	gi73299	Homo sapiens	apoptosis	2071	100
		79		regulator	405	100
466	4487	gi67066	Homo sapiens		405	100
4.55	4401	59 gi98373	Homo sapiens	CamKI-like	1044	100
467	4491	g1983/3 41	HOMO Saprens	protein kinase	1044	200
468	4492	Y42751	Homo sapiens	Human calcium	586	99
400	4432	132/31	nomo Baptons	binding		
j	1		1	protein 2	1	1
1	1			(CaBP-2).		<u> </u>
469	4497	q161797	Homo sapiens	<del>                                     </del>	352	37
1.22		40	1	paraneoplastic		
}	1	}	1	cancer-testis-	1	1
1		1		brain antigen	<u> </u>	
470	4502	gi63297	Homo sapiens	KIAA1124	327	100
1	1 _	42		protein		
471	4519	Y99426	Homo sapiens	Human PRO1604	1563	100
		1		(UNQ785) amino		
	1			acid sequence	4.000	<u> </u>
472	4526	X08008	Homo sapiens	Human HLIG-1	4023	99
			<u> </u>	protein.	1 43.65	
473	4547	gi45895	Homo sapiens	KIAA0959	4165	99
	1	62	Mara massarilas	protein	1164	77
474	4554	gi13810	Mus musculus		7703	1 ''
L		29	<u></u>	<u> </u>		L

					Smith	* 7
SEQ	SEQ ID	Acces- sion	Species	Description	Smith	Identity
NO:	NO:	No.			Water	zachozoy
1.01	in				man	
	USSN	}			Score	
	09/48					
]	8,725	J			<b>.</b>	
475	4555	gi27923	Homo sapiens	unknown	4461	99
		66		protein IT12		
476	457	Y70551	Homo sapiens	Human latent	1825	100
	ļ			transforming growth		
ļ	]	j		factor-beta	,	
	ļ			binding		
<b>i</b>	į			protein 3 (I).	` `	
477	4571	gi53601	Homo sapiens	NY-REN-45	869	100
		15	_	antigen		
478	4613	Y05868	Homo sapiens	Human Toll	2413	100
1				protein		
				PRO358.		
479	4614	Y27129	Homo sapiens	Human bone	1815	100
		1		marrow-derived		
				polypeptide (clone OAF038-		
				Leu).	1	
480	4622	G03789	Homo sapiens	Human	173	53
400	1022	003703	nomo sapiciis	secreted	1	
				protein,	ļ	[
481	4667	gi76736	Danio rerio	Dedd1	446	48
ł		38				
482	4670	gi40264	Homo sapiens	c-rel	2309	100
L		9				
483	4683	Y68773	Homo sapiens	Amino acid	2234	99
		{	ĺ	sequence of a human		
İ				phosphorylatio		
	1	1		n effector		
			,	PHSP-5.		
484	4698	¥73470	Homo sapiens	Human	746	100
				secreted		
1				protein clone		
ł		ł		yd141_1	i	
1				protein		
100	4704	-: 64565	Homo gandana	sequence hypothetical	1101	99
485	4724	gi64568 46	Homo sapiens	protein	1101	""
486	4734	gi33349	Homo sapiens	R27216 1	1151	80
1 -00	7/37	82	LISING Dapacing			
487	4814	gi62744	Homo sapiens	pregnancy-	1348	100
	-7	73		induced growth		]
1		1		inhibitor		
488	4819	Y07825	Homo sapiens	Human	117	67
1			[	secreted		
		1	1	protein		ļ
}				fragment #4 encoded from		
L	l	J	<u></u>	encoded trom	L	

	GRO		Cnocios	Description	Smith	8
SEQ ID	SEQ ID	Acces- sion	Species	Description	-	Identity
NO:	NO:	No.			Water	100110107
NO.	in	NO.			man	
	USSN	ļ		ŀ	Score	
	09/48			Ì		
	8,725					
	-,			gene 28.		
489	4821	Y81498	Homo sapiens	Human foetal	1200	100
				bone-derived		
		1		growth		
		•		factor-like	İ	
				protein.		
490	4851	gi56894	Homo sapiens	KIAA1077	4364	99
		91		protein	2.50	
491	4872	gi59119	Homo sapiens	hypothetical	3723	99
		53		protein		7.00
492	4902	B08917	Homo sapiens	Human	717	100
	1	[		secreted	1	
				protein sequence		
				encoded by		
	ļ	ļ		gene 27		
493	5006	gi43577	Homo sapiens	receptor	385	100
493	3000	9143377	nomo Bapieno	tyrosine		
		-		kinase isoform		
		۱ ،	•	FLT4 long,		
•				FLT41 {C-		
	1			terminal}	ļ	.
494	5007	Y93951	Homo sapiens	Amino acid	804	100
				sequence of a		
				Brainiac-5		l
				polypeptide.		
495	5027	gi35487	Homo sapiens	R33590_1	1606	100
400	5029	91 gi56895	Homo sapiens	KIAA1095	5722	99
496	5029	27	Homo sapiens	protein	3,22	
497	5033	Y14482	Homo sapiens	Fragment of	166	66
	3033	114402	nome paptens	human secreted		
				protein		
				encoded by		
				gene 17.		
498	5040	Y95019	Homo sapiens	Human	258	92
			•	secreted		]
				protein vql_1,		]
499	5061	gi13044	Pseudorabies	EP0	85	38
	l	34	virus			
500	5081	gi40380	Homo sapiens	vascular	134	100
		81		endothelial		]
				cell growth		
				inhibitor	0346	
501	5129	gi31691	Homo sapiens	BC269730_2	2340	99
	<del> </del>	58	Tions of the	LIDYTM1	293	47
502	5139	gi40628	Homo sapiens	HEXIM1 protein	293	*'
E00	F174	56	Homo sapiens	140up gene	576	90
503	5174	gi93685	nomo sapiens	Tannh derre	3,6	

CEO	CEO	Acces-	Species	Description	Smith	8
SEQ ID	SEQ ID	sion	Species	Description	-	Identity
NO:	NO:	No.			Water	
но.	in	]			man	
	USSN				Score	
	09/48					
	8,725					
		40		product	-555	
504	524	G00329	Homo sapiens	Human	565	100
				secreted protein,		ļ
505	5291	Y92515	Homo sapiens	Human OXRE-	1271	98
505	2231	192515	nomo sapiens	12.		]
506	5335	gi72961	Drosophila	CG3862 gene	753	46
300	3333	58	melanogaster	product	\	
507	5346	Y94987	Homo sapiens	Human	849	100
		Ì	_	secreted		<b>!</b>
}		1		protein vjl_1,		
508	5379	gi71445	Homo sapiens	cytokine-	1353	99
		06		inducible SH2-	1	[
				containing		l
				protein	1516	100
509	5441	gi80965	Homo sapiens	similar to mouse Ehm2	1210	100
<u> </u>	549	51 Y22113	Homo sapiens	Human ZSMF-3	294	62
510	549	122113	nomo saprems	protein	27.	"
{	Ì			sequence.		1
511	5542	¥76267	Homo sapiens	Fragment of	1066	100
			1	human secreted		
ł	Ì			protein		ļ [
ļ	ļ			encoded by		]
	<u> </u>			gene 11.	103	36
512	5560	G03790	Homo sapiens	Human secreted	103	30
				protein,		
513	5696	gi79203	Homo sapiens	PTOVI	1904	91
313	3050	98	nomo bapaono			
514	5704	B08930	Homo sapiens	Human	987	100
		1	_	secreted	}	]
ĺ				protein	[	
İ				sequence		
<b>\</b> .		1		encoded by		
	L	W1 6686	Yloma gardana	gene 2 Human protein	368	100
515	5758	W18878	Homo sapiens	kinase C	300	100
1			1	inhibitor,		
1				IPKC-1.	1	
516	5760	gi65621	Homo sapiens	hypothetical	425	100
		76	[	protein	1	
517	5763	Y41706	Homo sapiens	Human PRO381	441	100
				protein	1	
				sequence.		
518	5787	Y57907	Homo sapiens	Human	952	100
				transmembrane protein HTMPN-		
				protein HIMPN-		
L			<u> </u>	1	11	<u> </u>

				Donovintion	Smith	*
SEQ	SEQ	Acces-	Species .	Description	SMILLI	Identity
ID	ID	sion No.			Water	raciicity
NO:	NO: in	NO.			man	
!	USSN				Score	
!	09/48	1				
	8,725					
519	5823	gi98002	rat	pr5	153	36
	1	42	cytomegalovir			
			us Maastricht			
520	5886	gi17810	Mus musculus	neuronal	1135	52
		37		tyrosine		
				threonine		
				phosphatase 1	710	96
521	5924	W69221	Homo sapiens	Human parotid	1 /10	. 36
	ŀ	•	•	secretory protein.		}
	5060	Y91529	Homo sapiens	Human	1300	99
522	5960	131273	HOMO SAPTERS	secreted	1300	
	1			protein	<b>!</b>	Ì
				sequence	1	1
				encoded by		·
		1		gene 79		İ
523	5962	W69784	Homo sapiens	Protein	395	100
		ļ	_	Kinase C	}	ļ
				Inhibitor-like		
				Protein		
	_			(IPKC-2).		
524	5969	Y79141	Homo sapiens	Human	1205	79
	ļ			haemopoietic		
	Į.			stem cell regulatory		
				protein		
	•		ļ	SCM113.		ļ
525	5976	gi78031	Homo sapiens	natural	1808	91
525	33/8	0	nomo Bapieno	killer		
	1		}	associated	ļ	
			ĺ	transcript 4		Ì
526	6002	gi21045	Homo sapiens		4367	67
	}	53			l	
527	6008	Y66765	Homo sapiens	Membrane-	822	100
				bound protein	}	
l ·		l		PRO1384.		
528	6020	gi19115	Homo sapiens	cytochrome c-	322	50
		48		like		
  - <u>-</u>	1	1.17.2.2.2.		polypeptide Human	353	51
529	6036	W71362	Homo sapiens	cytokine/stero	333	""
		1	1	id receptor	1	
				protein.	Ī	
530	6070	Y42750	Homo sapiens	·Human calcium	626	100
330	3070	1 1 1 2 / 3 0		binding		
				protein 1		1
1			1	(CaBP-1).		
531	6075	gi10732	Homo sapiens	angiopoietin-	2164	100
1		648	_	like protein		

	650	( <b>.</b>		- Becamination	Smith	8
SEQ ID	SEQ ID	Acces- sion	Species	Description	-	Identity
NO:	NO:	No.	1		Water	
10.	in				man	
	USSN				Score	
	09/48					
Ì	8,725					
				PP1158	1240	
532	6106	gi22179 70	Homo sapiens	p40	1349	96
533	6420	W82000	Homo sapiens	Human adult	929	100
				brain secreted protein		
	}			dm26_2.		
534	6434	gi10732	Homo sapiens	angiopoietin-	2164	100
	1	648		like protein		
				PP1158		
535	6439	gi18970	Homo sapiens	endothelial	376	100
		1		cell growth		
536	6463	Y41720	Homo sapiens	Human PRO792	360	82
336	0403	141/20	110000 Sapiens	protein		52
{		Ì		sequence.		
537	6466	gi48840	Homo sapiens	hypothetical	538	100
ì <u> </u>	·	84		protein	<u></u>	
538	6508	gi54420	Homo sapiens		2317	96
		30	77	aminopeptidase	1591	99
539	6570	gi59214 91	Homo sapiens			
540	6719	gi31847	Homo sapiens	glypican	1625	87
541	6772	Y65432	Homo sapiens	Human 5' EST related	180	53
				polypeptide		
542	6789	gi53729	Homo sapiens	ICH-1L	1556	100
		2	_			
543	6805	gi44547	Homo sapiens	HSPC007	634	84
544	6833	02 qi18906	Homo sapiens	protein	5726	87
544	6633	60	Tomo saprens	tyrosine		
		"	1	phosphatase		
ļ				receptor		
				omicron		
545	6834	gi59214	Homo sapiens		1746	88
	6055	91	Homo sapiens	neuropilin	3968	98
546	6851	gi24076 41	nomo sapiens	Henrobitin	3900	30
547	6868	gi67146	Drosophila	MAP kinase	218	49
	]	41	melanogaster	phosphatase		
548	6876	Y13138	Homo sapiens	Human	414	76
[		1		secreted	1	
ĺ			1	protein		
				encoded by 5'		
549	688	Y73463	Homo sapiens	Human	701	98
				secreted		1
		1		protein clone		
L			<del></del>	1.5		<del></del>

SEQ	SEO	Acces-	Species	Description	Smith	ક
ID	ID	sion		-	<b>→</b>	Identity
NO:	NO:	No.	Į.		Water	
	in	ĺ			man	
	USSN	İ			Score	
	09/48					1
	8,725					l
				yk199_1		
	[			protein		
				sequence		
550	6897	gi58151 80	Homo sapiens	unknown	509	97
551	690	gi10645	Homo sapiens	meningioma-	522	100
	i .	186		expressed		
	,			antigen 5s	,	
	1			splice variant	l	
552	6909	W78149	Homo sapiens	Human	485	100
				secreted		
				protein	1	
		ı		encoded by		
•				gene 24 clone	}	
	_			HSVBF78.		
553	6924	Y35923	Homo sapiens	Extended	514	99
				human secreted		
				protein		
		l		sequence,		
554	6937	G03798	Homo sapiens	Human	281	70
ı	ł	1		secreted		1
<u> </u>	<u> </u>			protein,	364	95
555	6951	gi51185	Homo sapiens	prostate-	304	}
		7		specific antigen		Į
			Trama gandana	Human	548	98
556	7008	G03200	Homo sapiens	secreted	7 20	
		1		protein,	1	
	7000	Y22213	Homo sapiens	Human V201	856	100
557	7009	122213	HOMO Saprems	protein		
				sequence.		
558	7057	gi60036	Homo sapiens	brain	1814	100
228	1007	54	TOWN DAPTERS	specific		
		1 34	İ	membrane-		
				anchored	1	
				protein BSMAP		
559	7098	W27291	Homo sapiens	Human H1075-1	712	100
ر در	,			secreted		}
[				protein 5'		1
1				end.		
560	7114	gi32121	Homo sapiens	prefoldin	534	98
		10	}	subunit 1	1	}
561	712	gi45586	Homo sapiens	P85B_HUMAN;	470	74
	1	41	_	PTDINS-3-		
1			1	KINASE P85-		
		}		BETA		<u> </u>
562	7215	gi48683	Homo sapiens	delta-6 fatty	2437	100
		66		acid		
1	1	1		desaturase	}	i

SEQ   SEQ   Acces   Species   Description   Smith   Identify
NO:
in USSN 09/48 8,725   S63   7244   Y12445   Homo sapiens   Human 5' EST secreted protein   S64   7248   gi31137   Homo sapiens   Humig   G33   100   S65   7252   gi56895   Homo sapiens   KIAA1097   S240   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100
USSN   09/48   8,725   563   7244   Y12445   Homo sapiens   Human 5' EST   428   100   564   7248   gi31137   Homo sapiens   Humig   633   100   6   6   6   6   6   6   6   6   6
09/48   8,725   563   7244   Y12445   Homo sapiens   Human 5' EST   428   100
8,725
Total
Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Sequence   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted
Total
Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted   Secreted protein   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Se
Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl
31
Total   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Section   Sectio
98
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receptor molecule (REC) encoded by Incyte clone 2057886.  568 7338 Y73880 Homo sapiens Human prostate tumor EST fragment derived protein #67.  569 736 gil0178 Homo sapiens 317  570 737 G00851 Homo sapiens Human secreted protein,  571 740 W85610 Homo sapiens Secreted protein,  572 7400 Y93948 Homo sapiens Amino acid sequence of a lectin ss3939
molecule (REC)   encoded by   Incyte clone   2057886.
encoded by   Incyte clone   2057886.
Incyte clone 2057886.
2057886.
Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Tabl
prostate tumor   EST fragment   derived   protein #67.
EST fragment derived protein #67.  569 736 gil0178 Homo sapiens 1468 100  570 737 G00851 Homo sapiens Human 522 98 secreted protein,  571 740 W85610 Homo sapiens Secreted protein clone eh80_1.  572 7400 Y93948 Homo sapiens Amino acid sequence of a lectin ss3939
derived   protein #67.
569         736         gi10178 317         Homo sapiens         1468         100           570         737         G00851 Homo sapiens         Human secreted protein,         522         98           571         740         W85610 Homo sapiens         Secreted protein clone eh80_1.         1115         87           572         7400         Y93948 Homo sapiens         Amino acid sequence of a lectin ss3939         1982         98
569         736         gi10178   Homo sapiens         1468   100           570         737         G00851   Homo sapiens   Human secreted protein,         522   98           571         740   W85610   Homo sapiens   Secreted protein clone eh80_1.         1115   87           572         7400   Y93948   Homo sapiens   Amino acid sequence of a lectin ss3939         1982   98
570         737         G00851         Homo sapiens         Human secreted protein,         522         98           571         740         W85610         Homo sapiens         Secreted protein clone eh80_1.         1115         87           572         7400         Y93948         Homo sapiens         Amino acid sequence of a lectin ss3939         1982         98
Secreted   protein,
protein,
571   740   W85610   Homo   sapiens   Secreted   protein clone   eh80_1.
protein clone eh80_1.  572 7400 Y93948 Homo sapiens Amino acid 1982 98 sequence of a lectin ss3939
eh80_1.  572 7400 Y93948 Homo sapiens Amino acid 1982 98 sequence of a lectin ss3939
572 7400 Y93948 Homo sapiens Amino acid 1982 98 sequence of a lectin ss3939
sequence of a lectin ss3939
lectin ss3939
573 7415 gi30436 Homo sapiens KIAA0573 2392 100
70 protein
574 7429 Y40864 Homo sapiens A human 1183 99
glutathione-S-
transferase
(hGST)
575 7458 Y53643 Homo sapiens A bone marrow 554 99 secreted
protein
designated
BMS6.
576 7516 gi44683 Homo sapiens 1146 99
11
577 7526 gi41389 Homo sapiens promyelocytic 3571 99
leukemia zinc   finger

		3	Creater	Description	Smith	9
SEQ	SEQ	Acces- sion	Species	Describeron	- JIII - LII	Identity
ID NO:	ID NO:	No.	ļ		Water	
NO:	in	NO.			man	İ
1	USSN				Score	
	09/48					j
	8,725					
				protein;	-	
				kruppel-like		l
				zinc finger		
				protein; PLZF	200	100
578	7571	G02915	Homo sapiens	Human	209	100
				secreted protein,		
579	7614	W74726	Homo sapiens	Human	1879	100
579	/614	W/4/20	HOMO Saprens	secreted	1075	100
				protein		
				fg949_3.		
580	7663	gi59125	Homo sapiens	<del>_</del>	1634	100
		48	-		1	l l
581	7686	gi49297	Homo sapiens	CGI-121	870	100
		11		protein		
582	7714	gi38876	Homo sapiens	phospholipase	4428	99
		5		D		
583	7724	G03933	Homo sapiens	Human	570	100
				secreted		
			**	protein, mesenchymal	1133	100
584	7834	gi89191 66	Homo sapiens	stem cell	1133	100
•		66		protein DSC92		
585	7855	Y48505	Homo sapiens	Human breast	684	100
303	, 055	110302		tumour-		
				associated	j	
	j			protein 50.		
586	7870	Y13372	Homo sapiens	Amino acid	2559	100
		1		sequence of	}	
				protein	İ	1
	<u> </u>	<u> </u>		PRO223.	755	1 7 7 7 7
587	7871	Y91689	Homo sapiens	Human	768	100
İ				secreted		}
1				protein sequence		
·				encoded by	-	
!				gene 93		
588	7892	gi34659	Homo sapiens	macrophage	532	100
300				inflammatory		
				protein-2alpha		
1		ŀ		precursor		
589	7927	gi32575	Homo sapiens		183	91
590	7944	gi16574	Sus scrofa		2744	100
		58		calcium/calmod		
		1		ulin-dependent		
			<u> </u>	protein kinase		
ļ		1	[	II isoform	1	
	7047	G01131	Homo sapiens	gamma-B Human	574	96
591	7947	GOTTOT	Trout Saprens			1

SEQ ID NO:		<del></del>		Beggnerich	Smith	*
	SEQ	Acces-	Species	Description	- SIII.ECII	Identity
NO:	ID	sion No.			Water	,
	NO:	NO.			man	j
ĺ	in				Score	
- [	USSN				DCOLG	
	09/48				]	
	8,725			secreted	<del></del> -	
		i		protein,		
		220014	War cariona	neutral	167	68
592	800	gi30214	Homo sapiens	sphingomyelina	] -0,	
ļ		28	•	sphingomyerina	1	
			77	CGI-84	1038	100
593	8055	gi49296	Homo sapiens	protein	1030	100
		37		HSPC014	715	100
594	8082	gi46790	Homo sapiens	HSPC014	,13	100
l		14			905	95
595	8127	gi99556	Homo sapiens	twisted gastrulation	303	• 33
ł		93		protein	ļ	
				•	767	100
596	8174	gi55322	Homo sapiens	MUM2	/6/	100
		94			1111	100
597	8178	gi45305	Homo sapiens	TADA1 protein	1132	100
		87			<u> </u>	100
598	8215	R66278	Homo sapiens	Therapeutic	830	100
ļ	ļ			polypeptide	1	
. 1	ĺ		i	from	1	İ
	1			glioblastoma	Ī	<b>f</b>
	,			cell line.		
599	8263	Y48371	Homo sapiens	Human	713	98
				prostate		
	1		1	cancer-	1	
		]		associated	ł	
	l		· ·	protein 68.		
600	827	gi31723	Cavia	phospholipase	955	73
	1	37	porcellus	B	<u> </u>	
601	828	¥29517	Homo sapiens	Human lung	833	94
	ŀ		<u> </u>	tumour protein	1	1
	İ			SAL-82		
l .	ļ			predicted	ł	1
	ł			amino acid	ļ	
				sequence.		
602	8294	gi49297	Homo sapiens	sequence.	1085	100
602	8294	67		sequence. CGI-149 protein		
602	8294	1 -	Homo sapiens	sequence. CGI-149 protein group IID	1085	100
		67		sequence.  CGI-149 protein group IID secretory		
		67 gi57714		cGI-149 protein group IID secretory phospholipase		
		67 gi57714		sequence.  CGI-149 protein group IID secretory	852	100
		67 gi57714		sequence.  CGI-149 protein group IID secretory phospholipase A2 Human		
603	8313	67 gi57714 20	Homo sapiens	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted	852	100
603	8313	67 gi57714 20	Homo sapiens	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted protein	852	100
603	8313	67 gi57714 20	Homo sapiens	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted	852	100
604	8313	67 gi57714 20 Y86260	Homo sapiens	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted protein	852	100
603	8313	67 gi57714 20	Homo sapiens	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted protein HELHN47,	319	78
604	8313	9157714 20 Y86260 gi41913 58	Homo sapiens Homo sapiens Mus musculus	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted protein HELHN47,	319	78
604	8313 832 8357	9157714 20 Y86260	Homo sapiens	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted protein HELHN47, claudin-7	319	78
604	8313 832 8357	9141913 58 9119452	Homo sapiens Homo sapiens Mus musculus	sequence.  CGI-149 protein group IID secretory phospholipase A2 Human secreted protein HELHN47, claudin-7	319	78

SEQ	SEQ	Acces-	Species	Description	Smith	ક
ID	ID	sion	oper-or		_	Identity
NO:	NO:	No.			Water	-
NO:	in	1.0.			man	
	USSN				Score	
	09/48		•			
	8,725					
	8,723	81		cardiotrophin-		
		01		like cytokine	Į	
				CLC	Ĭ	[
608	8380	gi34022	Homo sapiens	protein	974	100
600	8380	16	nomo saprens	proces		
609	8386	gi38698	Homo sapiens	oncostatin M	1297	99
609	0300	8	nomo saprens	oncoboaca.		1
610	8418	Y70210	Homo sapiens	Human TANGO	722	98
010	0410	1,022	220	130 protein.	1	
611	8442	G01895	Homo sapiens	Human	490	95
011	0442	002033	110o Dup_0	secreted	ĺ	1
	1	i	<u> </u>	protein,	ļ	[
612	8457	G04048	Homo sapiens	Human	450	98
012	0437	904040	nomo bapiemo	secreted		
	1			protein,	ļ	
613	8458	W97119	Homo sapiens	S-adenosyl-L-	1484	100
θT2	0430	MAILLA	nomo saprens	methyltransfer		1
	1			ase (SAM-MT)	ı	
	l ·			protein.	l.	
	0460	gi71597	Homo sapiens	process.	255	100
614	8469	g1/159/	HOMO Sapiens		233	100
615	8480	gi45895	Homo sapiens	KIAA0943	1998	100
	}	30	_	protein		
616	8521	gi57262	multiple	unknown	250	82
		35	sclerosis	protein U5/2	1	
		1	associated			ļ
		1	retrovirus			
		}	element		1	
617	857	qi96639	Homo sapiens	cysteinyl	612	99
	1	58	_	leukotriene	1	
			1	CysLT2	l .	}
		1		receptor		
618	8574	gi68412	Homo sapiens	HSPC305	1049	100
		60	<u> </u>		ļ	·
619	8606	gi33677	Homo sapiens	scrapie	544	100
	1	07	İ	responsive	ļ	j
				protein 1	1	l
620	8632	G01158	Homo sapiens	Human	502	100
				secreted	İ	İ
	1			protein,		•
621	8646	gi38822	Homo sapiens	KIAA0764	2175	100
		49		protein	-	1
622	8666	Y66196	Homo sapiens	Human bladder	1080	95
				tumour EST		
			1	encoded		
	1	1		protein 54.	1	1
623	8675	gi99639	Homo sapiens	NPD009	432	96
023	33,3	08				1
624	8683	G04018	Homo sapiens	Human	469	98

SEQ	SEQ	Acces-	Species	Description	Smith	8
ID	ID	sion	Species	Descripcion	-	Identity
NO:	NO:	No.			Water	·
110.	in				man	}
	USSN			•	Score	
	09/48					]
	8,725					_
				secreted		
				protein,		
625	8708	gi16335 64	Homo sapiens	C8	364	98
626	8720	gi82484	Homo sapiens		191	69
	ł	65	-	hepatocellular	1	
·	ļ	}		carcinoma-		1
			-	associated	`	
				antigen 56A		
627	8756	Y94984	Homo sapiens	Human	369	97
ł		1		secreted	[	
]		j		protein	j	
L				vell_1,	1068	97
628	8765	¥00346	Homo sapiens	Fragment of human secreted	1008	"
		Ī		protein		1
		{		encoded by	<b>.</b>	{
1		1		gene 2.		
629	8783	Y27918	Homo sapiens	Human	1051	95
023	0,03	12/510	nome sapreme	secreted		
1	1	ļ		protein	1	1
		1		encoded by		
'	]			gene No. 123.	ļ	
630	8804	Y25426	Homo sapiens	Human SIGIRR	887	100
				protein.		
631	8838	Y99409	Homo sapiens	Human PRO1343	1279	100
				(UNQ698) amino		
<u></u>			ļ <u>.</u>	acid sequence	454	100
632	8851	W74785	Homo sapiens	Human secreted	*34	100
				protein		
1		ļ	<u> </u>	encoded by		1
				gene 56 clone	}	j ļ
1				HSAXS65.		1
633	8853	W75116	Homo sapiens	Human	245	95
			1	secreted		ļ
		-		protein		[
				encoded by		}
		1		gene 60 clone		
L				HILCJ01.	480	<del>  </del>
634	8857	gi25651	Homo sapiens	non-	479	74
1		96		functional		
				folate binding protein	}	1
-	1 0050	Y02690	Homo sapiens	Human	600	100
635	8859	102090	Tromo sabrens	secreted		
}	}	1	1	protein	}	
-				encoded by	1	1
				gene 41c lone		
ł	1	_L	<u> </u>	13 320		<u></u>

SEQ	SEQ	Acces-	Species	Description	Smith	<b>8</b>
ID	ID	sion	Species	Description	-	Identity
NO:	NO:	No.			Water	_
	in .				man	
	USSN				Score	
	09/48					
	8,725					
				HSZAF47.		
636	8901	Y86491	Homo sapiens	Human gene	548	99
	[			59-encoded		
			•	protein fragment,		}
637	8907	W88745	Homo sapiens	Secreted	2004	99
637	8907	W00/43	nomo sapiens	protein	1	
				encoded by	`	
				gene 30 clone		
	[			HTSEV09.		
638	8934	W75088	Homo sapiens	Human	421	98
			-	secreted		
		į į		protein		\$
	ĺ			encoded by		
		İ		gene 32 clone		i
				HAGBB70.		
639	8960	Y02693	Homo sapiens	Human	267	72
		1		secreted		
				protein encoded by		
				gene 44 clone		
	]	j		HTDAD22.		
640	8979	Y76143	Homo sapiens	Human	1374	98
	l		7	secreted		
				protein	1	
			,	encoded by		
				gene 20.		
641	8980	Y11433	Homo sapiens	Human 5' EST	466	100
	ļ	1	'	secreted		ļ.
	1	700505	77	protein Human	306	100
642	8986	G02626	Homo sapiens	secreted	300	100
		I		protein,		
643	8987	G02093	Homo sapiens	Human	486	97
043	0,50,	002033	nome buplone	secreted		1
				protein,	:	
644	8995	Y12908	Homo sapiens	Human 5' EST	181	100
	1	1	]	secreted	1	· ·
		]		protein		
645	9035	Y71108	Homo sapiens	Human	800	100
(		1		Hydrolase	Ì	
1	1			protein-6	1	
	<u> </u>			(HYDRL-6).		100
646	9062	gi88860	Homo sapiens	lysophosphatid	523	100
1		05	1	ic acid		
ı	1		<b>]</b> .	acyltransferas		
ļ.						
		1	İ	e-delta		

050	SEQ	Acces-	Species	Description	Smith	8
SEQ ID	ID	sion	phecies	Deactipaton	-	Identity
NO:	NO:	No.			Water	
но.	in				man	
	USSN				Score	l
	09/48					
	8,725					
				secreted		
				protein		
		Ì		encoded from		
'	Ì			gene 51.		
648	9075	¥73336	Homo sapiens	HTRM clone	1591	100
		ĺ		1852290	•	[
			•	protein	١.	
			***	sequence.	516	100
649	9098	¥57878	Homo sapiens	Human transmembrane	210	100
		,		protein HTMPN-		
		1		2.		
650	9109	gi23903	Homo sapiens	63kDa protein	1141	97
030		3		kinase	1	<b> </b>
651	911	gi32456	Homo sapiens	protein-	2591	100
ł		-		tyrosine		
		1		phosphatase		
652	912	gi11367	Homo sapiens	human P5	212	46
Ì		43				
653	9163	Y34129	Homo sapiens	Human	377	71
				potassium		
i ·		ĺ		channel K+Hnov28.		[
	0164	Y41324	Homo sapiens	Human	1083	99
654	9164	141324	HOMO Sapiens	secreted	1005	
				protein		
				encoded by		
1				gene 17 clone		ļ
				HNFIY77.		
655	9173	gi68512	Mus musculus	protein	631	93
1		56		tyrosine		
	•			phosphatase-		
				like protein		
				PTPLB	1173	05
656	9187	Y66721	Homo sapiens	Membrane-	11/3	95
				bound protein PRO511.	1	[
657	9190	W40378	Homo sapiens	Human breast	792	81
65′	9190	11-10-37-0	Daprens	cancer protein		
				CH14-2a16-1		[
ł			1	from 2.0 kB		[
				DNA fragment		[
			,	#2.	<u></u>	<u> </u>
658	9194	Y02781	Homo sapiens	·Human	462	70
1	1			secreted		<u>,</u>
<u> </u>	1			protein.		
659	9210	G02994	Homo sapiens	Human	166	80
			1	secreted		
1		<u></u>	<u> </u>	protein,	<u> </u>	1

SEQ	SEQ	Acces-	Species	Description	Smith	*
ID	ID	sion	Opecies	202022	_	Identity
NO:	NO:	No.			Water	•
NO.	in	1.0.			man	
	USSN	,			Score	
	09/48		}			ì
	8,725					ì
660	9222	G02520	Homo sapiens	Human	186	43
880	7222	002320	nomo supromo	secreted	ł	
		li	·	protein,		
661	9230	gi67065	Homo sapiens	inositol	1315	95
801	7230	54	Nome Dapage	1,4,5-		Į į
·	l	1		trisphosphate	<b>\</b>	
	1	1		3-kinase B	<b>!</b> ,	[ [
662	9258	gi52214	Homo sapiens	B-cell growth	120	56
002	7230	5	1100 20.71	factor		i i
663	9260	G04072	Homo sapiens	Human	138	51
003	7200	3010.2		secreted	l	1
		Ì		protein,	Į.	i l
664	9271	gi66900	Homo sapiens	tetraspanin	317	67
004	32/1	95	nomo bapzono	protein		}
665	9272	gi16304	Bos taurus	factor	444	72
603	3212	2	1	activating	1	
				exoenzyme S		}
666	9275	gi40177	Homo sapiens	ribosomal	424	81
000	3273	4	Nome Baptons	protein S6	ł	
				kinase 3	ł	
667	930	G02355	Homo sapiens	Human	167	41
337	] ""	002333		secreted		
1	<u> </u>			protein,	i	
668	9304	q189797	Canis	Band4.1-like5	1493	93
555	3301	43	familiaris	protein	1	
669	9346	gi27389	Mus musculus	high mobility	384	89
003	33.20	89		group protein		
				homolog HMG4		
670	9347	gi36613	Homo sapiens		199	91
{		1		serine/threoni		1
ł		ŀ	[	ne protein	1	ì
ł		ł		kinase	1	
671	935	gi55418	Homo sapiens	QA79 membrane	334	57
1		70	_	protein,		1
1.		1	Í	allelic		1
'		1		variant airm-		
1		1		1b		
672	9350	gi33271	Homo sapiens	KIAA0655	757	87
		24	1	protein		L
673	9351	W57260	Homo sapiens	Human	573	9.5
	1		1	semaphorin Y.		
674	9356	gi59977	Human	tripartite	127	59
	1		endogenous	fusion		1
1		1	retrovirus	transcript		1
	1			PLA2L		
675	9363	Y17834	Homo sapiens	Human PRO361	968	92
}	1	1	Į.	protein	}	1
1				sequence.	<b> </b>	1
676	9366	gi72431	Homo sapiens	KIAA1374	649	96

OHO.	SEQ	Acces-	Species	Description	Smith	
SEQ ID	ID	sion	Species	Description	- 5	Identity
NO:	NO:	No.			Water	200110407
NO.	in	1.0.			man	
	USSN				Score	
	09/48					
	8,725					•
		29		protein		
677	9369	G03793	Homo sapiens	Human	222	69
	1			secreted	ł	
				protein,		
678	9378	gi44683	Homo sapiens		163	39
		11				
679	9393	gi27389	Mus musculus	high mobility	384	89
	<u> </u>	89	·	group protein	1	
			<u></u>	homolog HMG4	1.52	93
680	9444	G01399	Homo sapiens	Human	157	93
			}	secreted	}	,
	2467	-144547	Were engine	protein, HSPC007	230	71
681	9467	gi44547	Homo sapiens	HSPC007	230	/-
682	9486	gi10047	Homo sapiens	KIAA1584	605	93
002	] ,,,,,	243	,	protein		
683	949	Y30895	Homo sapiens	Human	704	99
			1	secreted		
1	]		}	protein		,
				fragment		ļ
		1		encoded from	1	
		}		gene 25.		
684	9499	W36002	Homo sapiens	Human Fchd531	2173	96
	<u> </u>			gene product.		
685	9510	gi16657 99	Homo sapiens		867	83
686	9523	Y53022	Homo sapiens	Human	1252	89
	]			secreted		
	Ì	}		protein clone		j
	ł	Į.		qf116_2		ļ
	ŀ			protein	j	ļ
			· · · · · · · · · · · · · · · · · · ·	sequence Membrane-	998	100
687	9534	Y66670	Homo sapiens	bound protein	220	100
	-		ì	PRO1180.	Ì	
688	9539	Y76144	Homo sapiens	Human	633	100
] , ,	"	1,0144		secreted	}	
				protein		
)		1	]	encoded by		
1	1	1		gene 21.	1	1
689	954	G02490	Homo sapiens	Human	160	78
1		1		secreted	1	}
		-	[	protein,	<u> </u>	<u> </u>
690	9546	gi18112	Homo sapiens	chorionic	616	96
		1	1	somatomammotro		1
L		<u> </u>		pin	1	
691	955	gi72431	Homo sapiens	KIAA1361	2042	100
	<del> </del>	03		protein	341	E7
692	9551	gi17723	Homo sapiens	ras-related	341	57

SEQ	SEQ	Acces-	Species	Description	Smith	8
ID	ID	sion	bpccicb	Bubulle	-	Identity
NO:	NO:	No.			Water	
NO.	in	NO.			man	1
	USSN				Score	Į.
	09/48					ļ
	8,725					1
	0,123	45		GTP-binding	<del>                                     </del>	
				protein	]	
693	9558	W88403	Homo sapiens	Human adult	2252	100
		ļ	<u>.</u>	testis		1
				secreted		
			,	protein		, ,
		<u> </u>	ı	ga63_6.	,	]
694	9561	gi66900	Herpesvirus	NTR	100	30
	ļ	17	papio			
695	957	Y86260	Homo sapiens	Human	319	78
		l	ļ	secreted	ļ	
	Ì	ľ		protein	[	1
		i	Ì	HELHN47,		
696	9572	gi97294	Mus musculus	Elf-1	806	92
	1	0			<u> </u>	
697	9576	gi32490	Homo sapiens	geminin	448	98
		05		<u> </u>		
698	9586	gi28872	Homo sapiens	mRNA cleavage	208	100
		88		factor I 25		1
		_		kDa subunit		
699	9587	G00995	Homo sapiens	Human	726	99
				secreted	1	
				protein,		
700	9592	gi49527	Rattus	ribosomal	202	78
		3	norvegicus	protein S15a	1-153	
701	9595	gi77999	Homo sapiens	UBASH3A	453	47
		12	<u> </u>	protein Human	574	100
702	9610	Y07875	Homo sapiens	secreted	3/4	100
		]		protein	}	}
	}	1		fragment		
)	1	1		encoded from		}
Ì				gene 24.		ļ
707	9634	Y73325	Homo sapiens	HTRM clone	820	99
703	7034	1/3323	TOUG Sapters	001106 protein	""	1
ļ ·	1		1	sequence.		1
	0630	G00805	Homo sapiens	Human	155	67
704	9639	900803	TOWO Saprens	secreted		"
1				protein,		
705	9647	G03786	Homo sapiens	Human	196	73
/ / / 3	704/	303788	Tomo adviena	secreted		
	1			protein,		]
706	9653	gi38823	Homo sapiens	KIAA0810	523	100
,,,	7033	41		protein		
707	9654	G01924	Homo sapiens	Human	469	100
/ / /	"	332524		secreted		
1		1		protein,	1	1
708	9678	Y99376	Homo sapiens	Human PRO1244	474	100
, , ,	) 3376			(UNQ628) amino	-	1
	<u> </u>			(UNQ628) amino	<u></u> _	<u> </u>

To   No: No: No.	CTIO 1	SEQ	Acces-	Species	Description	Smith	
NO: NO: NO: 11 USSN 09/48 8,725	-		i .	apecies	Descripcio	_	-
in USSN 09/48 8,725		_	1	•		Water	
USSN   9748   8,725	NO.					man	
09/48						Score	
8,725						1	
			l i			·	
Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted protein   Secreted pr					_		
Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Prot	709	9709	Y11825	Homo sapiens		657	100
710   9722   gi76774   Mus musculus   GTPase Rab37   189   75     711   9731   Y12424   Homo sapiens   Human 5' EST secreted protein     712   9742   Y57954   Homo sapiens   Human transmembrane protein HTMPN-78     713   9749   gi36878   Homo sapiens   hT41   386   65     714   9755   gi20552   Homo sapiens protein in cosmid C14H10     715   9762   G03436   Homo sapiens protein in cosmid C14H10     716   9763   gi61800   Homo sapiens   Human secreted protein,     717   9784   G03570   Homo sapiens   Human secreted protein,     718   9794   G00803   Homo sapiens   Human secreted protein,     719   9795   gi25162   Mus musculus   Rab33B   69   94     720   9798   gi55859   Homo sapiens   SIMILAR   Human secreted protein,     721   9805   Y25881   Homo sapiens   Human secreted protein with interaction domain     722   9816   gi53205   Homo sapiens   Protein-   384   100     722   9816   gi53205   Homo sapiens   Protein-   384   100     722   9816   gi53205   Homo sapiens   Protein-   384   100     722   9816   gi53205   Homo sapiens   Protein-   384   100     723   724   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725   725							
711   9731   Y12424   Homo sapiens   Human 5   EST secreted protein	710	9722	, -	Mus musculus	GTPase Rab37	189	75
Secreted   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Protein   Pro				*****	Theman El Dem	207	100
	711	9731	Y12424	Homo sapiens	}	201	100
712   9742   Y57954   Homo sapiens   Human transmembrane protein HTMPN-78.   386   65     713   9749   gi36878   Homo sapiens 29   Homo sapiens   Similar to a C.elegans protein in cosmid C14H10     715   9762   G03436   Homo sapiens   Human secreted protein,   176   61     716   9763   gi61800   Homo sapiens   Human secreted protein,   177   9784   G03570   Homo sapiens   Human secreted protein,   717   9784   G00803   Homo sapiens   Human secreted protein,   718   9794   G00803   Homo sapiens   Human secreted protein,   719   9795   gi25162   Mus musculus   Rab33B   669   94     720   9798   gi55859   Homo sapiens   ZID, zinc finger protein with interaction domain   721   9805   Y25881   Homo sapiens   Human secreted protein finger protein fingent encoded from gene 61.   722   9816   gi53205   Homo sapiens   Protein   384   100							
transmembrane protein HTMPN-78.  713 9749 gi36878 Homo sapiens hT41 386 65  714 9755 gi20552 Homo sapiens Similar to a C.elegans protein in cosmid C14H10  715 9762 G03436 Homo sapiens Human secreted protein,  716 9763 gi61800 Homo sapiens anaphase-promoting complex subunit 4  717 9784 G03570 Homo sapiens Human secreted protein,  718 9794 G00803 Homo sapiens Human secreted protein,  719 9795 gi25162 Mus musculus Rab33B 669 94  720 9798 gi55859 Homo sapiens ZID, zinc finger protein with interaction domain  721 9805 Y25881 Homo sapiens Human secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein protein fragment encoded from gene 61.		0.74.7	752054	Vere garriera		494	100
Protein HTMPN-78.	712	9742	15/954	nomo sapiens	_ · · · · · · · · · · · · · · · · · · ·	***	100
78			i I			Ì	
713   9749   gi36878   Homo sapiens   hT41   386   65     714   9755   Gi20552   Homo sapiens   Similar to a   2583   100     715   9762   G03436   Homo sapiens   Human   secreted   protein,     716   9763   gi61800   Homo sapiens   anaphase-   promoting   complex   subunit   4     717   9784   G03570   Homo sapiens   Human   secreted   protein,     718   9794   G00803   Homo sapiens   Human   secreted   protein,     719   9795   gi25162   Mus musculus   Rab33B   669   94     720   9798   gi55859   Homo sapiens   ZID, zinc   finger protein   with   interaction   domain     721   9805   Y25881   Homo sapiens   Human   secreted   protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   finger protein   fing			<b>'</b>			1	
10	712	9749	gi 36878	Homo saniens	' - '	386	65
S	/13	3143	, -	nomo bapieno			
	714	9755	gi20552	Homo sapiens	1	2583	100
Cosmid C14H10   To			95				
715   9762   G03436   Homo sapiens   Human secreted protein,		ł	Ì			}	
Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted	ļ .		l			<u> </u>	
	715	9762	G03436	Homo sapiens	l .	176	61
716   9763   gi61800   Homo sapiens   anaphase-promoting complex subunit 4     717   9784   G03570   Homo sapiens   Human secreted protein,     718   9794   G00803   Homo sapiens   Human secreted protein,     719   9795   gi25162   Mus musculus   Rab33B   669   94     720   9798   gi55859   Homo sapiens   ZID, zinc finger protein with interaction domain     721   9805   Y25881   Homo sapiens   Human secreted protein fragment encoded from gene 61.     722   9816   gi53205   Homo sapiens   protein   384   100     722   9816   gi53205   Homo sapiens   Protein   384   100     731   732   733   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table   Table	1		1	•		İ	
11   promoting complex subunit 4	<u>.</u>					1000	
	716	9763		Homo sapiens		1016	100
Subunit 4			1 11				
717 9784 G03570 Homo sapiens Human secreted protein,  718 9794 G00803 Homo sapiens Human secreted protein,  719 9795 gi25162 Mus musculus Rab33B 669 94  720 9798 gi55859 Homo sapiens ZID, zinc finger protein with interaction domain  721 9805 Y25881 Homo sapiens Human secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein— 384 100	Ì	ĺ		İ			
Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted   Secreted	777	9794	G03570	Homo saniens	<u> </u>	401	96
	/1/	3/04	003370	nomo saprens	1		
718   9794   G00803   Homo sapiens   Human   333   69     719   9795   Gi25162   Mus musculus   Rab33B   669   94     720   9798   Gi55859   Homo sapiens   ZID, zinc   605   96     9	ļ						
Secreted protein,	718	9794	G00803	Homo sapiens	<del></del>	333	69
719 9795 gi25162 Mus musculus Rab33B 669 94  720 9798 gi55859 Homo sapiens ZID, zinc 605 96  9 finger protein with interaction domain  721 9805 Y25881 Homo sapiens Human 566 96  secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100		1			secreted		
720 9798 gi55859 Homo sapiens ZID, zinc 605 96  9 finger protein with interaction domain  721 9805 Y25881 Homo sapiens Human 566 96  secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100		ŀ			protein,		
720 9798 gi55859 Homo sapiens ZID, zinc 605 96 finger protein with interaction domain  721 9805 Y25881 Homo sapiens Human 566 96 secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100	719	9795	gi25162	Mus musculus	Rab33B	669	94
finger protein with interaction domain  721 9805 Y25881 Homo sapiens Human 566 96 secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100			1				
with   interaction   domain	720	9798	1 -	Homo sapiens	ZID, zinc	605	96
interaction domain  721 9805 Y25881 Homo sapiens Human 566 96 secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100			9		1 -		[
domain	j		l .				]
721 9805 Y25881 Homo sapiens Human 566 96 secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100					i -		
secreted protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100			1.0====			666	96
protein fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100	721	9805	Y25881	nomo sapiens	l	300	96
fragment encoded from gene 61.  722 9816 gi53205 Homo sapiens protein- 384 100	ļ	1		}		1	ł
encoded from gene 61.			1			1	
	1	!	1	1		1	
722 9816 gi53205 Homo sapiens protein- 384 100	1				•		
1 744 1 3444 1 3444 1 1 4	722	9816	gi53205	Homo sapiens		384	100
6	1 /22	5310	6		tyrosine-	1	
phosphatase			1				j
723 9830 G00857 Homo sapiens Human 539 96	723	9830	G00857	Homo sapiens		539	96

	SEQ	Acces-	Species	Description	Smith	8
SEQ ID	ID	sion	Species	Descripcion	-	Identity
NO:	NO:	No.			Water	
1.0.	in				man	
-	USSN				Score	
	09/48	ļ			1	
	8,725	1				[
				secreted		
				protein,		
724	9836	G00914	Homo sapiens	Human	527	100
		ļ		secreted	}	
				protein,		67
725	9837	gi26620	Homo sapiens	KIAA0409	230	6/
	- 004	99	770	Human lung	833	94
726	984	Y29517	Homo sapiens	tumour protein	033	94
j	j			SAL-82		
		]		predicted		
	ļ	<u> </u>		amino acid		
)		1		sequence.	}	
727	9849	gi72293	Homo sapiens	ZNF264,	140	90
		05	•	partial cds		}
728	9851	gi52625	Homo sapiens	hypothetical	369	64
İ	İ	60		protein	1	
729	9859	gi38819	Homo sapiens	hypothetical	167	93
		76		protein		
730	9863	gi72957	Drosophila	CG15433 gene	837	78
		07	melanogaster	product		
731	9888	gi33196	Homo sapiens		209	72
732	000	77 gi45571	Rattus	zinc finger	604	92
/32	989	43	norvegicus	protein RIN ZF	004	, ,,,
733	9919	G01843	Homo sapiens	Human	586	100
/33	وعود	001043	nomo bapieno	secreted		
			·	protein,	j	}
734	9922	W67869	Homo sapiens	Human	551	93
			_	secreted		
				protein		
}		1		encoded by		
1				gene 63 clone		
	<u> </u>			HHGDB72.		
. 735	9947	W78239	Homo sapiens	Fragment of	251	78
1				human secreted	j	
	1		[	protein encoded by		
1		j		gene 3.		}
736	9956	Y36203	Homo sapiens	Human	273	77
1,30	9930	130203	110mo Baptens	secreted		
j		1		protein #75.		1
737	9961	Y99357	Homo sapiens	Human PRO1190	650	99
1		1		(UNQ604) amino	1	1
j			]	acid sequence		<u> </u>
738	9972	Y12149	Homo sapiens	Human 5' EST	284	100
1				secreted		
				protein		<u> </u>
739	9977	gi10039	Homo sapiens	osteoblast	822	98

SEQ	SEQ	Acces-	Species	Description	Smith	ક
ID	ID	sion	_		-	Identity
NO:	NO:	No.			Water	
1	in	1			man	
}	USSN				Score	
1	09/48	1				1
1	8,725	i i				
		439		differentiatio		
{				n promoting	Ì	ļ
ĺ		1		factor		

## Table 3 - Amino Acids

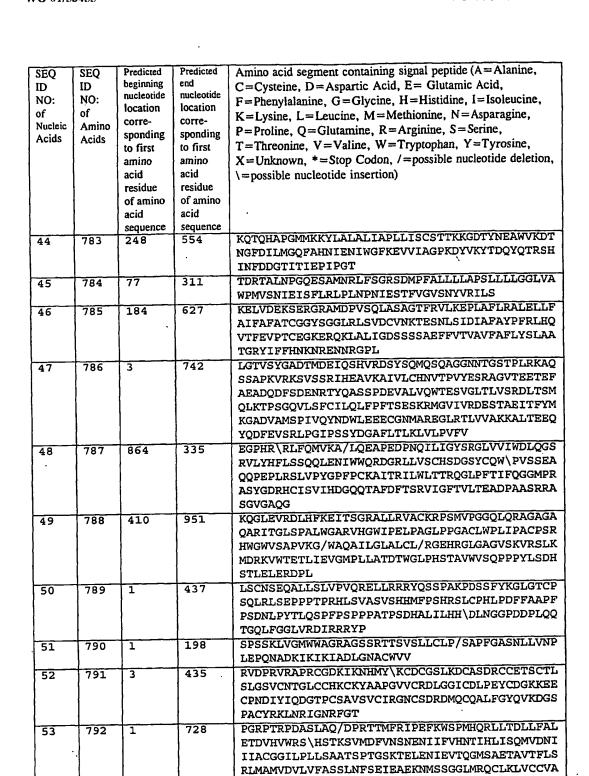
SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide insertion)
1	740	2	557	FVGRLLRLGEALRLRPDPSGGCRLQPALVGETEMSEKENNFPP
		1		LPKFIPVKPCFYQNFSDEIPVEHQVLVKRIYRLWMFYCATLGV
1				NLIACLAWWIGGGSGTNFGLAFVWLLLFTPCGYVCWFRPVYKA
				FRADSSFNFMAFFFIFRSPVCPDRHPGDWLLRLGRVRLAVGNW
	<u>L</u>			ILPVQPGRCRGHA
2	741	305	838	FLGAGADIFCAYLRMSSKQATSPFACAADGEDAMTQDLTSREK
			-	EEGSDQHVASHLPLHPIMHNKPHSEELPTLVSTIQQDADWDSV
ł	l	}	Į.	LSSQQRMESENNKLCSLYSFRNTSTSPHKPDEGSRDREIMTSV
· ·		1		TFGTPERRKGSLADVVDTLKQKKLEEMTRTEQEDSSCMEKLLS
	L			KDWKE
3	742	12	1315	EGYLTGRPTRPVAVRGKSTADLRMMGRSPGFAMQHIVGVPHVL
1		1		VRRGLLGRDLFMTRTLCSPGPSQPGEKRPEEVALGLHHRLPAL
}	1		}	GRALGHSIQQRATSTAKTWWDRYEEFVGLNEVREAQGKVTEAE
	}		ļ	KVFMVARGLVREAREDLEVHQAKLKEVRDRLDRVSREDSQYLE LATLEHRMLQEEKRLRTAYLRAEDSEREKFSLFSAAVRESHEK
	<b>l</b>			ERTRAERTKNWSLIGSVLGALIGVAGSTYVNRVRLQELKALLL
			1	EAQKGPVSLQEAIREQASSYSRQQRDLHNLMVDLRGLVHAAGP
		1		GODSGSOAGSPPTRDRDVDVLSAALKEQLSHSRQVHSCLEGLR
		1		EQLDGLEKTCSQMAGVVQLVKSAAHPGLVEPADGAMPSFLLEQ
1		{	ĺ	GSMILALSDTEORLEAQVNRNTIYSTLVTCVTFVATLPVLYML
			1	FKAS
	743	112	745	NLPPLTPQPGPRLAGSGPSHWFSPLSLPVASKAPGTMAQALGE
4	/43	112	/45	DLVQPPELQDDSSSLGSDSELSGPGPYRQADRYGFIGGSSAEP
			'	GPGHPPADLIRQREMKWVEMTSHWEKTMSRRYKKVKMQCRKGI
				PSALRARCWPLLCGAHVCQKNSPGTYQELAEAPGDPQWMETIG
		1		RDLHROFPLHEMFVSPQGHGQQGLLQVLKAYTLYRPEQG
5	744	99	265	LRGMAAAAAGPAASQRFFQSFSDALIDQDPQAALEVGEPFLLP
	'33	-		PLPADPPPSSTA
1	1 _	· I · · · · · · · · · · · · · · · · · ·		

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID ID	ID ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	F=Pnenylaianine, G=Glycine, H=Histidine, I=Isoleuchie,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
110103	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
1		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	,
		of amino	of amino	
	•	acid	acid	
		sequence	sequence	
6	745	210	758	WACFRSAHCSRHLRNRIFMYLYWDKTRSPVCKGPALREERPQP
		1		RLKLEDYKDRLKSGEHLNPDQLEAVEKYEEVLHNLEFAKELQK
		•	ł	TFSGLSLDLLKAQKKAQRREHMLKLEAEKKKLRTILQVQYVLQ
		Ì	ì	NLTQEHVQKDFKGGLNGAVYLPSKELDYLIKFSKLTCPERNES
		}		LROTLEGSTV
7	746	48	450	XAGVQMKLEFLQRKFWAATRQCSTVDGPCTQSCEDSDLDCFVI
′	, 30	10	-50	DNNGFILISKRSRETGRFLGEVDGAVLTQLLSMGVFSQVTMYD
		1		YQAMCKPSSHHHSAAQPLVSPISAFLTATRWLLQELVLFLLEW
	Ì	į.	<b>[</b>	SVWGSX*
		<del></del>	469	CRGRLAQLEEAAVAATMSAGDAVCTGWLVKSPPERKLQRYAWR
8	747	1	469	KRWFVLRRGRMSGNPDVLEYYRNKHSSKPIRVIDLSECAVWKH
Į į		1		
				VGPSFVRKEFQNNFVFIVKTTSRTFYLVAKTEQEMQVWVHSIS
			<u> </u>	QVCNLGHLEDGAADSMESLSYTRSYLQ
9	748	242	409	IPAVPLTSCVTVGSYSLSVRDYDPRQGDTVKHYKIRTL\DKRG
·	Ì		1	FYISP\RSTFSTLQ
10	749	1.	1146	KDSVLNIARGKKYGEKTKRVSSRKKPALKC/TSQKQPALKAIC
	İ	į	ļ	DKEDSVPNTATEKKDEQISGTVSSQKQPALKATSDKKDSVSNI
		Ì		PTEIKDGQQSGTVSSQKQPAWKATSVKKDSVSNIATEIKDGQI
ŀ	l		i	\RGTVSSQRQPALKA\TGDEKDSVSNIAREIKDGEKSGTVSPQ
l		1	ì	KQSAQKVIFKKKVSLLNIATRITGGWKSGTEYPENLPTLKATI
	ļ	ł	1	ENKNSVLNTATKMKDVQTSTPEQDLEMASEGEQKRLEEYENNQ
		}	}	PQVKNQIHSRDDLDDIIQSSQTVSEDGDSLCCNCKNVILLIDQ
		1	1	HEMKCKDCVHLLKIKKTFCLCKRLTELKDNHCEQLRVKIRKLK
			Į	NKASVLQKRLSEKEEIKSQLKHETLELEKELCSLRFAIQQ
11	750	3	892	SPLRYRAGOSGSTISSSSCAMWRCGGRQGLCVLRRLSGGHAHH
	/30	1	1 322	RAWRWNSNRACERALOYKLGDKIHGFTVNQVTSVPELFLTAVK
ļ	ĺ	1	1	LTHDDTGARYLHLAREDTNNLFSVQFRTTPMDSTGVPHILEHT
{	ł		1	VLCGSQKYPCRDPFFKMLNRSLSTFMNAFTASDYTLYPFSTQN
ł	İ			PKDFQNLLSVYLDATFFPCLRELDFWQEGWRLEHENPSDPQTP
ļ	<b>j</b>	1		LVFKGVVFNEMKGAFTDNERIFSQHLQNRLLPDHTYSVVSGGD
}	]	}		
	<del> </del>	1-0-E-	1055-	PLCIPELTWEQLKQFHATHYHPSNARFFTYGNFPLDQH RGAKAKSAVLPPGPPCSSILILSPPAPLTPRSPGTEATRPTAM
12	751	367	856	
1	1	1	-	SKSLKKKSHWTSKVHESVIGRNPEGQLGFELKGGAENGQFPYL
1	1	1	1	GEVKPGKVAYESGSKLVSEELLLEVNETPVAGLTIRDVLAVIK
1		1	<u></u>	HCKDPLRLKCVKQGESSGLLSVLPGGGTARGAGQ
13	752	144	442	SHRPQPDAWRQGNAFQCVQKEKMQVSSAEVRIGPMRLTQDPIQ
	1			VLLIFAKEDSQSDGFWWACDRAGYRCNIARTPESALECFLDKH
]				HEIIVIDHRQTQN
14	753	1	581	FRLAGCGHLLVSLLGLLLLLARSGTRALVCLPCDESKCEEPRN
1	1	-		CPGSIVQGVCGCCYTCASQRNESCGGTFGIYGTCDRGLRCVIR
1				PPLNGDSLTEYEAGVCEDENWTDDQLLGFKPCNENLIAGCNII
1	1			NGKCECNTIRTCSNPFEFPSQDMCLSALKRIEEEKPDCSKARC
1				EVOFSPRCPEDSVLIEGYAPP
1				

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No: of of Nucleic location of Nucleic location of Nucleic Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acids   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Admin Acid   Adm		-			Amino acid segment containing signal peptide (A-Alainie,
Not of Nucleic   Not of Amino   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acids   Acid	1 1				C=Cysteine, D=Aspartic Acid, E= Glutainic Acid,
Acids Acids Sponding to first amino acid residue of amino acid residue of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior of amino acid sequence superior superior of amino acid sequence superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior superior su	1 1			location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
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amino acid sequence  15 754 1 219 FRMAANVGSMPQYWKRFDLQQLQRELDATATVLANRQDESEQS RKRLLEGSREFKNTFBVRRVTIVFALKGS  16 755 313 562 ETISCRIMDHPSRRKDERQRTTRFMAQRSAHGSRPSGSSSSG VLMVGPNRVGKKIGCONFGELRLGGELPQVYYFGPCGKY  17 756 273 574 GCCKD+HSGVIGSWANLFASGGFQVKLYDIEQQLINALENI RWASKRSPEGMEVGLFLSVGLVCHILKAWRICUVTFSDGVCS ASELVKARPTVAGM  18 757 3 390 NSRVDDFVSARPKPRPLPRARGMVVVTGREPDSRRQDGAMSS DAEDDFLEFATPTATQAGHAL/PPAAT/GSFLRLFPLTSEGLT SLHACPHGGATKTPCWQPCSVGGTTSPRTPRAGTSSTEMAHTLEMC  19 758 98 461 RALWVGGCSGEACGIGMSGLLTDPEQRAQEPRYPGFVLGLDVG SSVIRCHVYDRAARVCSSVQKVENLYDCIGWELDPDVLMIQ FVAVIKEAVRAGIGYMNGIVGLGISTQATFITW  20 759 100 731 GLAAEQSMQFVKLWGCSGFPTRLRRRTPLTFAMEGGPAVCC QOPRAELVERVAADITYMQIVGLGISTQATFITW  21 760 2 520 FVYGKPVTLWPTISSVVPSTFLGLGNYEVEVEAEQAGFYATGP ASHISPRAWRRPTISSHVAISDAEDCVQLNQYKLQSEIGKGA YGVVLAVIMSEDRHYMKVLJSKKLKLKQVGFPRRPPP  22 761 158 470 SLAMPFGCVTLGKKNYNQPSEVTDRYDLGJFTRGFRPP  23 762 1 749 QRRFRFGKLTGKKYNKQPSEVTDRYDLGJFTRAGTKSFK IELLARCDGVSDCKDGEDEYXCVEVGGQNAALQVFTAASRKIM QLUVPLXNHSTEDRETYTLGLIGHTPCSSKVRCRSSFK IELLARCDGVSDCKDGEDEYXCVEVGGQNAALQVFTAASRKIM CLUPVTRKEYFIFLEL  23 762 1 749 QRRFRFGKLHTCKKFQKRDGRKVRKAAKNBIGILKMVKHPNIL QLUDVFVTRKEYFIFLEL  24 763 3 558 SCFKGRTGGRGSGSGBSWARCGRHFSASTESPPLSQPTREMMLKFYSFY KQATEGPCKLSRPGFWDPIGRYKKNASSLGGMFSASEEBEAC  24 763 3 558 SCFKGRTGGRGSGSGSTWARCGRHFSASTESPPLSQPTSCALLDMILKFYSFY KQATEGPCKLSRPGFWDPIGRYKKNASSLGGMFSASEEBEAC  25 764 9 424 ESRERSGRRGAEDGSTVLLEGRCLVVCEGGRAAAGGPGSTAL	1 -		1	sponding	
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DLGNVLTSTPNAKTVNGKAESSDSGAESEEEAC  24 763 3 558 SCFKGRTGGRSGSSGDSSRWARCGRHFSASTEEPPLSQPCSAL PRSGRRGCAVPSSVTKMLSFFRRTLGRRSMRKHAEKERLREAQ RAATHIPAAGDSKSIITCRVSLLDGTDVSVDLPKKAKGQELFD QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSP YCLHLRVKFYSS  25 764 9 424 ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG		1		ł	~
24 763 3 558 SCFKGRTGGRSGSSGDSSRWARCGRHFSASTEEPPLSQPCSAL PRSGRRGCAVPSSVTKMLSFFRRTLGRRSMRKHAEKERLREAQ RAATHIPAAGDSKSIITCRVSLLDGTDVSVDLPKKAKGQELFD QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSP YCLHLRVKFYSS 25 764 9 424 ESRERSGNRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG		1			
PRSGRRGCAVPSSVTKMLSFFRRTLGRRSMRKHAEKERLREAQ RAATHIPAAGDSKSIITCRVSLLDGTDVSVDLPKKAKGQELFD QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSP YCLHLRVKFYSS 25 764 9 424 ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG			l	<u> </u>	
RAATHIPAAGDSKSIITCRVSLLDGTDVSVDLPKKAKGQELFD QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSP YCLHLRVKFYSS 25 764 9 424 ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG	24	763	3	558	
QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSP YCLHLRVKFYSS 25 764 9 424 ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG		1			
YCLHLRVKFYSS  25 764 9 424 ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG					
25 764 9 424 ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG				1.	QIMYHLDLIESDYFGLRFMDSAQVAHWLDGTKSIKKQVKIGSP
PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG				1	
	25	764	9	424	ESRERSGNRRGAEDRGTCGLQSPSAMLGAKPHWLPGPLHSPGL
A A T CEN DECENTED A RICE CHUTTED A CETCH CTCCA TVETO(IT.IN)	1	1	1		PLVLVLLALGAGWAQEGSEPVLLEGECLVVCEPGRAAAGGPGG
	-		1	I	AALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVN
EGGGFDRAS		1			EGGGFDRAS

SEQ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID .	ID	beginning nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino			P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids •	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
,		to first	to first	
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	
		of amino	of amino	
		acid	acid	•
		sequence	sequence	
26	76,5	2	507	EDVKSYYTVHLPQLENINSGETRTISHFHYTTWPDFGVPQSPA
			1	SFLNFLFKVRESGSLNPDHGPVVIHRSAGTGRSSTFSVVHTCL
			İ	VLMEKGDDINIKQVLLNIRKFQMGLI\QTPDQLRFSYMAITEG
			}	AKCVKGDSSIQKRWKELSKE/DLPPAFDHSPNKIMTEKYNR
27	766	84	852	LNRQRCGDQVLVPGTGLAAILRTLPMFHDEEHARARGLSEDTL
				VLPPASRNORILYTVLECQPLFDSSDMTIAEWVCLAQTIKRHY
			]	EQYHGFVVIHGTDTMAFAASMLSFMLENLQKTVILTGAQVPIH
			{	ALWSDGRENLLGALLMAGQYVIPEVCLFFQNQLFRGNRATKVD
				ARRFAAFCSPNLLPLATVGADITINRELVRKVDGKAGLVVHSS
			i	MEODVGLLRLYPGIPAALVRAFLOPPLKGVVMETFGSGNG
	767	992	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSL
28	/6/	992	210	I
			-	AARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEEPGPG
			ļ	ADGAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCL
			1	EVCRQSCQMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDV
				FFEPEDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALL
	'			YKWDMKCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKD
				SL
29	768	23	624	SFIYKHTHRARFGPRAIVASPALTAGPHVSLTASCRVGMWVSC
			1	SPSPFLHPTNTLVAVLERDTLGIREVRLFNAVVRWSEAECQRQ
			İ	QLQVTPENRRKVLGKALGLIRFPLMTIEEFAAGNRARAQGLVW
			-	EGSGTQVGIW/CTEDSAPEFTAESLADAWHIQIGRNLACEDAS
			1	T/WAIC*PRPGSVPTVHTARPRLSCLSSCF
30	769	100	2	MASTQDAELAVSRXRAIALXPGXQSXXPSQKKK
31	770	158	1957	LLKSCGVLLSGVCIPCEGKGPTVLVIQTAVPQDRPTKSSMRSA
				AKPWNPAIRAGGHGPDRVRPLPAASSGMKSSKSSTSLAFESRL
				SRLKRASSEDTLNKPGSTAASGVVRLKKTATAGAISELTESRL
			<b>\</b>	RSGTGAFTTTKRTGIPAPREFSVTVSRERSVPRGPSNPRKSVS
				SPTSSNTPTPTKHLRTPSTKPKQENEGGEK\VRLSPK/FRELL
			1	AEAKAKDSEINRLRSELKKYKEKRTLNAEGTDALGPNVDGTSV
			1	<del></del>
				SPGDTEPMIRALEEKNKNFQKELSDLEEENRVLKEKLIYLEHS
			1	PNSEGAASHTGDSSCPTSITQESSFGSPTGNQLSSDIDEYKKN
			]	IHGNALRTSGSSSSDVTKASLSPDASDFEHITAETPSRPLSST
			}	SNPFKSSKCSTAGSSPNSVSELSLASLTEKIQKMEENHHSTAE
			1	ELQATLQELSDQQQMVQELTAENEKLVDEKTILETSFHQHRER
			}	AEQLSQENEKLMNLLQERVKNEEPTTQEGKIIELEQKCTGILE
			<u> </u>	QGRFEREKLLNIQQQLTCSLRKVEEENQGALEMIKRLKEENEK
			ļ	LNEFLELERHNNNMMAKTLEECRVTLEGLKMENGSLKSHLQG
32	771	203	514	SOMHRLIFVYTLICANFCSCRDTSATPQSASIKALRNANLRRD
26				ESNHLTDLYRRDETIOVKGNGYVOSPRFPNSYPRNLLLTWRLH
		1	1	[
			L	SOENTRIOLVFDNQFGL

CEC T	SEO.	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ ID	SEQ ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
110103	Acius	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
[		residue	residue	,
		of amino	of amino	
	,	acid	acid	•
l }		sequence	sequence	
33	772	59	713	PFKKMTDLLRSVVTVIDVFYKYTKQDGECGTLSKGELKELLEK
[			1	ELHPVLKNPDDPDTVDVIMHMLDRDHDRRLDFTEFLLMIFKLT
]				MACNKVLSKEYCKASGSKKHRRGHRHQEEESETEEDEEDTPGH
				KSGYRHSSWSEGEEHGYSSGHSRGTVKCRHGSNSRRLGRQGNL
				SSSGNQEGSQKRYHRSSCGHSWSGGKDRHGSSSVELRERINKS
]			1	HIK
34	773	209	601	VPKISGPDHIDFIPWDQLFMASSSSVTEFLVLGFSSLGELQLV
	_	-		LFAVFLCLYLIILSGNIIIISVIHLDHSLHTPMYFFLGILSIS
				EIFYTTVILPKMLINLFSVFRTLSFVSCATQMFYEIVGPGTQE
		]	)	R
35	774	373	987	DHSTETPGIPAAEPVSHGTGKLERAPTLPAGAELPAPAAVPCP
33	,,,	3.3		TL*VC/LYPOLLGLSVATMVTLTYFGAHFAVIRRASLEKNPYQ
1		ļ	ļ	AVHQWGTQQRLIQHPESGSEGQSLLGPLRAFSAGLSLVGLLTL
1 1			Ì	GAVLSAAATVREAOGLMAGGFLCFSLAFCAQVQVVFWRLHSPT
1			i •	QVEDAMLDTYDLVYEQAMKGTSHVRRQELAAIQ
125-1	775	102	466	QPGYSEYDKNRGQGMLLNMMCGRQLSAISLCLAVTFAPLFNAQ
36	//5	102	400	ADEPEVIPGDSPVAVSEQGEALPQAQATAIMAGIQPLPEGAAE
] ' }		1		KARTQIESQLPAGYKPVYLNQLQLLYAARGISCSV
	776	<u> </u>	430	RTRAADVYVFSLTGKSRNVSSSTVRRSAVGGMSALALFDLLKP
37	776	2	430	NYALATQVEFTDPEIVAEYITYPSPNGHGEVRGYLVKPAKMSG
			ļ	KTPAVVVVHENRGLNPYIEDVARRVAKAGYIALAPDGLSSVGG
ļ		l	Į.	
				YPGNDIKVVSAAA
38	777	106	556	VKQRHGNSLLTTETKCISCRLGVPLSPQRRFQAIRIEEVKLRW
1			Į	FAFLIVLLAGCSSKHDYTNPPWNAKVPVQRAMQWMPISQKAGA
}	į		ļ	AWGVDPQLITAIIAIESGGNPNAVSKSNAIGLMQLKASTSGRD
<u> </u>				VYRRMGWSGEPTTSELKNSSR
39	778	3	892	HAAGIRHEAKPKRSFYAARDLYKYRHQYPNFKDIRYQNDLSNL
				RFYKNKIPFKPDGVYIEEVLSKWKGDYEKLEHNHTYIQWLFPL
1	i	l	Ì	REQGLNFYAKELTTYEIEEFKKTKEAIRRFLLAYKMMLEFFGI
		ì	1	KLTDKTGNVARAVNWQERFQHLNESQHNYLRITRILKSLGELG
		1		YESFKSPLVKFILHEALVENTIPNIKQSALEYFVYTIRDRRER
		ļ	j	RKLLRFAQKHYTPSENFIWGPPRKEQSEGSKAQKMSSPLASSH
	}	1	}	NSQTSMHKKAKDSKNSSSAVHLNSKTAEDKKVAPKEPV
40	779	123	395	ELQVFQPIGGMSDSGSQLGSMGSLTMKSQLQITVISAKLKENK
	ļ -			KNWFGPSPYVEVTVDGQSKKTEKCNNTNSPKWKQPLTVIVTPV
	[		1	SKLH
41	780	173	438	IETLSFVIRNWNTHAMSKPIVMERGVKYRDADKMALIPVKNVA
**	1 .55			TEREALLRKPEWMKIKLPADSTRIQGIKAAMRKNGLHSVCEEA
1	ļ		1	SC SC
1	707	287	393	PRMVLGKPQTDPTLEWFLSHCHIHKYPSKSTLIPQ
42	781	·	1	GLRISVQERIKACFTESIQTQIAAAEALPDAISRAAMTLVQSL
43	782	119	556	·
•		,	1	LNGNKILCCGNGTSAANAQHFAASMINRFETERPSLPAIALNT
1			Į.	
		}	ł	DNVVLTAIANDRLHDEVYAKQVRALGHAGDVLLAISTRGNSRD IVKAVEAAVTRDTTIV



VRNCLECRORORDRGNKSSHGSSKPQEVPQSVTATAASKTPLE

NVPGNLSPIKDPDRLLQDVDINRLRAVVF

				<u> </u>
SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
54	793	2230	990	NSSGVKLLQALGLSPGNGKDHSILHSRNDLEEAFIHFMGKGAA AERFFSDKETFHDIAQVASEFPGAQHYVGGNAALIGQKFAANS DLKVLLCGPVGPKLHELLDDNVFVPPESLQEVDEFHLILEYQA GEEWGQLKAPHANRFIFSHDLSNGAMNMLEVFVSSLEEFQPDL GGLSGLHMMEGQSKELQRKRLLEVVTSISDIPTGIPV\HLELG \SMTNRELMSSIV\LQQVFPAVTSLGLNEQELLFLTQSASGPH SSLSSWNGVPDVGMVSDILFWILKEHGRSKSRASDLTRIHFHT LVYHILATVDGHWANQLAAVAAGARVAGTQACATETIDTSRVS LRAPQEFMTSHSEAGSRIVLNPNKPVVEWHREGISFHFTPVLV CKDPIRTVGLGDAISAEGLFYSEVHPHY
55	794	249	3	DDSSGWGLEOLVVRWSLALWPRLECSGMISAHCNLCL/LGSSD SPASAPRVAGITDVCHHAWLVFVFLVVMGFPHVGHVGLELL
56	795	2	1176	LGEVLKCQQGVSSLAFALAFLQRMDMKPLVVLGLPAPTAPSGC LSFWEAKAQLAKSCKVLVDALRHNAAAAVPFFGGGSVLRAAEP APHASYGGIVSVETDLLQWCLESGSIPILCPIGETAARRSVLL DSLEVTASLAKALRPTKIIFLNNTGGLRDSSHKVLSNVNLPAD LDLVCNAEWVSTKERQQMRLIVDVLSRLPHHSSAVITAASTLL TELFSNKGSGTLFKNAERMLRVRSLDKLDQGRLVDLVNASFGK KLRDDYLASLRPRLHSIYVSEGYNAAAILTMEPVLGGTPYLDK FVVSSSRQGQGSGQMLWECLRRDLQTLFWRSRVTNPINPWYFK HSDGSFSNKQWIFFWFGLADIRDSYELVNHAKGLPDSFHKPAS DPGS
57	796	755	374	YHAPALQPGQQSKTLSQEKKNFFRPGAVAHTCNPSTLGGRGGR ITRSGDRDHPG*HGETPSLLKIQKKLAGRDGGRL*SQLLGRLR QENGVNPGGGGCSEPRLRHCTPAW*QSETISRKKRKKERKY
58	797	2	476	FRPIGIIRQALCSADGHQRRILTLRLGLLVIPFLPASNLFFRV GFVVPSVGCCVMLLFGFG/ALRKHTEKKKLIAAVVLGILLS/N DAERLRCAVRGGEWRSE/EAVFRGAVSVCPLSAEVRCNIGRNL AAKGNQTGAIRYHREAVSLNPKTKSSTREFRPC
59	798	3	711	KIADFGFSNLFTPGQLLKTWCGSPPYAAPELFEGKEYDGPKVD IWSLGVVLYVLVCGALPFDGSTLQNLRARVLSGKFRIPFFMST ECEHLIRHMLVLDPNKRLSMEQICKHKWMKLGDADPNFDRLIA ECQQLKEERQVDPLNEDVLLAMEDMGLDKEQTLQSLRSDAYDH YSAIYSLLCDRHKRHKTLRLGALPSMPRALGLSSTSQYP\AEQ AGTAMNISVPQVQLINPENQIV
60	799	2	344	AREFLGHRASITWS*ARVHHRFPKAEVA*P/SLLRTDLTEDRT KCCHGDLLECADDRADLVEDIWENQDSISTILIECCEKPLLEK SHCIAEVENDEMPADLPSLAADFVESKDV

050	000	Donalisand	Predicted	
SEQ	SEQ	Predicted beginning	end	Amino acid segment containing signal peptide (A=Alanine,
ID NO:	ID NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	
	1	residue	residue	\=possible nucleotide insertion)
ļ	1	of amino	of amino	
			acid	
1	ĺ	acid		·
	L	sequence	sequence 594	VPPKMKRGTSLHSRRGKPEAPKGSPQINRKSGQEMTAVMQSGR
61	800	142	394	1
ł			Į	PRSSSTTDAPTGSAMMEIACAAAAAAACLPGEEGTAERIERL
ļ	ļ	ł		EVSSLAQTSSAVASSTDGSIHTDSVDGTPDPQRTKAAIAHLQQ
l	l	ĺ		KILKLTEQIKIAQTARRNRRPGS*KDCTP*KCLRKSDEALNRV
}	1	}	}	LQQI\RVPPKMKRGTSLHSRRGKPEAPKGSPQINRKSGQEMTA
]	]	]	}	VMQSGRPRSSSTTDAPTGSAMMEIACAAAAAAAACLPGEEGTA
1	1			ERIERLEVSSLAQTSSAVASSTDGSIHTDSVDGTPDPQRTKAA
1	i	1		IAHLQQKILKLTEQIKIAQTARRNRRPG
62	801	232	1299	MOTIERLVKERDDLMSALVSVRSSLADTOOREASAYEOVKOVL
				QISEEANFEKTKALIQCDQLRKELERQAERLEKELASQQEKRA
ļ	ļ		Ì	IEKDMMKKEITKEREYMGSKMLILSQNIAQLEAQVEKVTKEKI
ĺ			{	SAINQLEEIQSQLASREMDVTKVCGEMRYQLNKTNMEKDEAEK
ĺ		ł	•	
		ł		EHREFRAKTNRDLEIKDQEIEKLRIELDESKQHLEQEQQKAAL
		ļ	ļ	AREECLRLTELLGESEHQLHLTRQEKDSIQQSFSKEAKAQALQ
{	ļ	(	ĺ	AQQREQELTQKIQQMEAQHDKTENEQYLLLTSQNTFLTKLKEE
		į.	İ	CCTLAKKLEQISQKTRSEIAQLSQEKRYTYDKLGKLQRRNEEL
·	l			EEQCVQHGRST*
63	802	3	334	SYPVWWNSPLTAEVPPELLAAAGFFHTGHQDKVRCFFCYGGLQ
	1			SWKRGDDPWTEHAKWFPSCQFLLRSKGRDFVHSVQETHSQLLG
	1			SWDPWEEPEDAAPVAPSVPASGYPELPTPRREVQSESAQEPGG
1	ł	Į.	ł	VSPAEAQRAWWVLEPPGARDVEAQLRRLQEERTCKVCLDRAVS
}		J	ļ	IVFVPCGHLVC\AECAPGLQLCPI\CRSPCGPLRPCLWVP
64	803	70	456	MCSYREKKAEPQELLQLDGYTVDYTDPQPGLEGGRAFFNAVKE
" -	***	1		GDTVIFASDDEQDRILWVQAMYRATGQSHKPVPPTQVQKLNAK
	1	į.	İ	GGNVPOLDAPISOFYADRAOKHGMDEFISSNPCNFDHASLFEM
1				*
- E	004	2	1376	KOLIVLGNKVDLLPQDAPGYRQRLRERLWEDCARAGLLLAPGH
65	804	4	13/6	
	1	ļ		QGPQRPVKDEPQDGENPNPPNWSRTVVRDVRLISAKTGYGVEE
	]	1		LISALQRSWRYRGDVYLVGATNAGKSTLFNTLLESDYCTAKGS
	1		1	EAIDRATISPWPGTTLNLLKFPICNPTPYRMFKRHQRLKKDST
1	1		1	QAEEDLSEQEQNQLNVLKKHGYVVGRVGRTFLYSEEQKDNIPF
1	1			EFDADSLAFDMENDPVMGTHKSTKQVELTAQDVKDAHWFYDTP
ł	ł			GITKENCILNLLTEKEVNIVLPTQSIVPRTFVLKPGMVLFLGA
1	1		1	IGRIDFLQGNQSAWFTVVASNILPVHITSLDRADALYQKHAGH
	]		1	TLLQIPMGGKERMAGFPPLVAEDIMLKEGLGASEAVADIKFSS
1	1			AGWVSVTPNFKDRLHLRGYTPEGTVLTVRPPLLPYIVNIKGOR
	1			IKKSVAYKTKKPPSLMYNVRKKKGKINV
	1005	<del> </del>	074	
66	805	1	874	STVASMMHRQETVECLRKFNARRKLKGAILTTMLVSRNFSAAK
{			1	SLLNKKSDGGVKPQSNNKNSLVSPAQEPAPLQTAMEPQTTVVH
			l	NATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEGRSSRD
1	1			RTAPSAGMQPQPSLCSSAMRKQEIIKITEQLIEAINNGDFEAY
				TKICDPGLTSFEPEALGNLVEGMDFHKFYFENLLSKNSKPIHT
1	[		1	TILNPHVHVIGEDAACIAYIRLTQYIDGQGRPSNPAKSEE\TR
1	1		}	VWH\RR\DGKWLNVHYHCSGAPCPHRCSELSHRGF
E .				

SEQ SEQ Predicted Predicted Ar	nino acid segment containing signal peptide (A=Alanine,
10 10 0.	=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
location location	Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Marine   Corre-   Corre-   IN-	=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acide Acide   sponding   sponding   P=	Proline, Q=Glutamine, R=Arginine, S=Serine,
to first to first T=	Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
amino amino X	=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	possible nucleotide insertion)
residue residue	<b>,</b>
of amino of amino	!
acid acid	
sequence sequence	
-	KNVVFVLDSSASMVGTKLRQTKDALFTILHDLRPQDRFSII
	SNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGAL
	AIRLLNKYVAHSGIGDRRVSLIVFLTDGKPTVGETHTLKIL
NN	TREAARGQVCIFTIGIGNDVDFRLLEKLSLENCGLTRRVHE
1 1 1 1	DAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFPNY
FN	GSEIIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRP
OF	AGKDVTGSPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQS
	EPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRMDGLEE
	GMSAAMGPEPVVQSVRGAGTQPGPLLKKPYQPRIKISKTSV
	DPHFVVDFPLSRLTVCFNIDGQPGDILRLVSDHRDSGVTVN
GE	LIGAPAPPNGHKKORTYLRTITILINKPERSYLEITPSRVI
1 1 1 1 1 1	OGGDRLVLPCNQSVVVGSWGLEVSVSANANVTVTIQGSIAFV
	.IHLYKKPAPFORHHLGFYIANSEGLSSNCRVFCESGILIQE
1 1 1 1 1	COSVAVAGR
	LEQVSQYTFAMCSYREKKSEPQELMQLEGYTVDYTDPHPGL
1 - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GCMFFNAVKEGDTVIFASDDEQDRILWVQAMYRATGQSYKP
1 1 1 1 1~	PAIOTOKLNPKGGTLHADAQLYADRFQKHGMDEFISANPCKL
	AFLFRILQRQTLDHRLNDSYSCLGWFSPGQVFVLDEYCARY
, , , , , , , , ,	RGCHRHLCYLAELMEHSENGAVIDPTLLHYSFAFCAS\HVH
	RPDGIGTVSVEEKERFEEIKERLSSLLENQISHFRYCFPFG
1 1 1	PEGALKATLSLLERVLMKDIA
	LLHEVLNGLLDRPDWEEAVKMPVGILPCGSGNALAGAVNQH
	FEPALGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSF
1 1 1 1 1 1 1	VAWGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYRGR
, , , , , , ,	SYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMAHSPLHR
1 1 1 1 1 1 1 1	STLPATVEPASPIPARSHPRARSHHITTPDFAPPRARSHMANSPINA SDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAG
	APLSPDPQLSSPPGSPKAALHSPV*KKAPVIPPDM
1 1 1 1	EVPTLLMAAGSFYDILAITGFNTCLGIAFSTGSTVFNVLRGV
	AT THE REGGE INTHATIGENIC COGENER GOOD LANGUAGE
	™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™™
LI	EVVIGVATGSVLGFFIQYFPSRDQDKLVCKRTFLVLGLSVLA
Li	SSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW
LI	rssvhfgfpgsgglctlvmaflagmgwtsekaevekiiavaw rfqpllfglig\aevsi\sslrpetvglcvatvgi\avliri
LI VI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF
71 810 228 541 LI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF KEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI
71 810 228 541 LI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW IFQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF .KEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER
71 810 228 541 LI St	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW IFQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF IKEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER IWNFGYWALWSPGNGC
71 810 228 541 LI St 72 811 173 404 IC	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW IFQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF IKEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER IWNFGYWALWSPGNGNGC TTSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW
71 810 228 541 LI St SI 72 811 173 404 IC	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF KEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER HWNFGYWALWSPGNGC TTSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW RYISDPNVD/ACPDPRNAEVSMTHTVPALMELID
71 810 228 541 LI St SI 72 811 173 404 IC CT 73 812 2 586 LI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF KEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER HWNFGYWALWSPGNGC TTSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW RYISDPNVD/ACPDPRNAEVSMTHTVPALMELID ESLPGFKEIVSRGVKVDYLTPDFPSLSYPNYYTLMTGRHCEV
71 810 228 541 LI St 72 811 173 404 IC 73 812 2 586 LI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF KEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER HWNFGYWALWSPGNGNGC TSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW RYISDPNVD/ACPDPRNAEVSMTHTVPALMELID ESLPGFKEIVSRGVKVDYLTPDFPSLSYPNYYTLMTGRHCEV QMIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLWVTLTK
71 810 228 541 LI ST SI SI CI CI CI CI CI CI CI CI CI CI CI CI CI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF LKEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER HWNFGYWALWSPGNGNGC TSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW RYISDPNVD/ACPDPRNAEVSMTHTVPALMELID ESLPGFKEIVSRGVKVDYLTPDFPSLSYPNYYTLMTGRHCEV DMIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLWVTLTK KRKVYMYYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSD
71 810 228 541 LI ST SI SI CI CI CI CI CI CI CI CI CI CI CI CI CI	FSSVHFGFPGSGGLCTLVMAFLAGMGWTSEKAEVEKIIAVAW FQPLLFGLIG\AEVSI\SSLRPETVGLCVATVGI\AVLIRI DYIF KEVVVQASPVCKTCCSQLVRTPVTFTEVQNV/CRCSAGYLI VCSYTSSDHNQCYAGTASLALLWIGGILKGCLLWKQFRWTER HWNFGYWALWSPGNGNGC TSTYLQIFPGKPSCFMCKGRLMCIYFILWYLGHYTSLHWNW RYISDPNVD/ACPDPRNAEVSMTHTVPALMELID ESLPGFKEIVSRGVKVDYLTPDFPSLSYPNYYTLMTGRHCEV QMIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLWVTLTK

CEC.	CEC	Predicted	Predicted	A mine said comment of the said and the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the said of the sa
SEQ	SEQ ID	beginning	end	Amino acid segment containing signal peptide (A=Alanine,
ID NO:	NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acius	Acias	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	t-possiole nacional insertion)
	,	of amino	of amino	
		acid	acid	
		sequence	sequence	
74	813	2	348	ARDFHPKQTLDFLRSDMANSKITEEVKRSIAQQYLDLTVA/LE
				QVDPDAEVDAAPSTTSSCGH*DSHAGS*RVLSLLGD*GPA*TG
		1	[	ANSMAGKLLLVAWLGFPDPFWGKELSDPAFK
75	814	2	366	KOSGDVTCNCTDGRLAPSCLTCVGHCIFGGYCTMNSKMMPECQ
		į		SPPHMTGPRCEEHVFSQHQPGHITSILIPML*LLLLVLVAGVI
		Ì	}	FCHKRRVOGAKGFOHORMTNGAMNAQIANPTYKMY
76	815	420	681	TVENAGRWL*EEAEIOAELERLERVRNLHIRELKRINNEDNSQ
, ,	013	120	**-	FKDHPTLNERYLLLHLLGRGGFSEVYKVMYGLFWFFYTNVARI
77	816	37	428	MCEEFLVMGKGCSCVF*ILLSNPOMWWLNDSNPETDNROESPS
, , , , , , , , , , , , , , , , , , ,	310	1 3 /	120	OENIDRVSD/MAFVPSAWTASGGVAWGNLGESGSRTGGVRAET
		f		LAPRLOV*PAHLRGHPRSNRGOGRPPWKAGKLGKCQEVLFRFA
		•		AF
78	817	1	358	FRAMFLAVOHDCRPMDKSAGSGHKSEEKREKMKRTLLKDWKTR
/8	81/	} +	330	LSYFLONSSTPGKPKTGKKSKQQAFIK*VENPELANINS*LLN
		1	1	*KGEL**A*ANIONLSCRPSPEEAOLWSEAFDE
		1	169	GFFNFSSPKLKGWKINSSLVLEIRKNILRFLDAERDVSVVKSS
79	818	-	103	FPSKDARHSSVHR*FTQLHWGPPSHTPARP*RGFFNFSSPKLK
· !		1	ĺ	
			1	GWKINSSLVLEIRKNILRFLDAERDVSVVKSSFPSKDARHSSV
	-	<del> </del>	330	HR
80	819	55	310	RIDDQQELKRVT*YSQKEYTKKKLHKKCNIIQADIKPDNILDN
				ESITILKLSDFGSASHVADNDITPSSSQTTSAASSPPRTLRR
81	820	1	134	SSKPWD*SLAPKHSG*TKNMDCYCIIPTCIGRERCYGTCIGDT
		<del> </del>		V
82	821	187	360	NSSKKLVMEHQWKKYLRRNYQRMLNRLITLIGSCGVL*LISTI
	İ	1		PTSRLKFLKETGHGTPMEEIPEEELSEDVEQIDHADRELRRGQ
L	L	L	<u> </u>	NLRCKGIHRLPTHIQVGQN
83	822	208	723	KWMLLHSFKIFCLSLYPQL*CPFEFFSHSATIFHELVYKQTKI
<u> </u>				ISSNQELIYEGRRLVLEPGRLAQHFPKTTEENPIFVVSREPLN
ļ	1		1	TIGLIYEKISLPKVHPRYDLDGDASMAKAITGVVCYACRIAST
]			L	LLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLGFLVSR
84	823	1	314	GTRKMGPTVSPICLPGTWGDYNLMDGDLGLISGWGRTEKRDRA
,	1			DRLKAGRSPAAG*RKWEPGRGDPTWEESEEDVHKSKWTRCVDE
	ŀ			KGA*C*TDNKRPLRCGVT
85	824	3	302	HELENLIKSAHSYSLY*G*YLHGA*TAEPEASFCPRRGWNRQA
l	1	1	l	GAAGSRMNFRPGVLSSRQLGLPGPPDGPDYTVYYPFHRLAMVT
1			1	AASRLEREHLTHL
86	825	87	422	PVPLPHPILEVCPGQ*EPQSAISLTAFQVQAGASRASPGPPAP
ļ	j	1	}	SSSKPGRKAKVASPCPDRPAPPPT*PRPAAAPGSESSPRPPRP
		1		RTGRRQQRAHARRAAARTAPWRPSC
87	826	3	289	HEGRRRGWASASQRFLRNWAFLTPSKVRRLKGQKAFGKLPSHS
1		_		DTSLTSDLGFHHRFNPNASSSFKPSGTKFAIQYGTGRVDGILS
ł	ì	ł		EDKLTVSGL
I	1			
88	827	1	101	GRNIMHYPNGHAICIANGHCIIL*NSHNIKVWV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, _possible nucleotide insertion)
89	828	1	535	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQH LFAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLL DRLHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETP RTSDGEKTLIEKMFGGKLRTHIRCLNCTSTSQKVEAFTDLSLA FWPSSS
90	829	1	434	ARDDPRVRLSLSPNFF*LASKLGKQWTPLIILANSLSGTNMGE
91	830	3	782	MHRIKLNDRMTFFEELDMSTFIDVEDEKSPQTESCTDSGAENE GSCHSDQMSNDFSNDDGVDEGICLETNSGTEKISKSGLEKNSL IYELFSVMVHSGSAAGGHYYACIKSFSDEQWYSFNDQHVSRIT QEDIKKTHGGSSGSRGYYSSAFASSTNAYMLIYRLKDPARNAK FLEVDEYPEHIKNLVQKERELEEQEKRQREIERNTCKIKLFCL HPTKQVMMED*IEVHKDKTLKEAVEMAYKMMDLEEVIPLDCCR L
92	831	2	604	SVMPVPALCILWALAMVTRPASAAPMGGPELAQHEELTILFHG TLQLGQALNGVYRTTEGRLTKARNSLGLYGRTIELLGQEVSRG RDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQKVLR DSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHV QRQRREMVAQQHRLRQIQERLHTAALPA
93	832	16	690	ITSVDPRVRGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGN NDCSHSEDVGVICSDASDMELRLVGGSSRCAGKVEVNVQGAVG ILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMS NSGCAGGEASLWDCIRWEWKQTACHLNMEASLICSAHRQPRLV GADMPCSGRVEVKHAHTWRSVCDSDFSLHAANVLCRELNCGDA ISLSVGDHFG
94	833	108	727	SNYPSSRFRVAGITGVKLGMRSIPIATACTIYHKFFCETNLDA YDPYLIAMSSIYLAGKVEEQHLRTRDIINVSNRYFNPSGEPLE LDSRFWELRDSIVQCELLMLRVLRFQVSFQHPHKYLLHYLVSL QNWLNRHSWQRTPVAVTAWALLRDSYHGALCLRFQAQHIAVAV LYLALQVYGVEVPAEVEA/DEAVGWQIYAMDTEIP
95	834	118	376	RGSRHAVHGWAFGLLFINKESVVMAYLFTTFNAFQGVF1FVFH CALQKKVRSRRGPGSQPPLETFPGYPGEGGEGGGDSGAPSSPQ
96	835	3	333	ARKDDLPPNMRFHEEKRLDFEWTLKAG*EKG*PSK*NKGWEGQ E***TVRD*GIS**VKPQHLS*\ALQMALKRVYTLLSSWNCLE
		740	951	DFDQIFWGQKSALAGQWFPEVSIIP GKQQRETLRPSPTISVQRAGSPEHSSASH*HSPCPAPGQRVL

SEQ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	согге-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic Acids	Amino   Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acius	Acius	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
!	ł	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	Ì	acid	acid	\=possible nucleotide insertion)
		residue	residue	
		of amino	of amino	
	l	acid	acid	•
	-	sequence	sequence 1503	GVCGLPRFCGSIILCHYEMSSLGASFVQIKFDDLQFFENCGGG
98	837	81	1503	SFGSVYRAKWISQDKEVAVKKLLKIEKEAEILSVLSHRNIIQF
İ		1		YGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWA
1	}	1		TDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGA
1				SRFHNHTTHMSLVGTFPWMAPEVIQSLPVSETCDTYSYGVVLW
1	1		1	EMLTREVPFKGLEGLQVAWLVVEKNERLTIPSSCPRSFAELLH
Ì	ļ			QCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEW
ļ				RCEIEATLERLKKLERDLSFKEQELKERERRLKMWEQKLTEQS
			ļ	NTPLLLPLAARMSEESYFESKTEESNSAEMSCQITATSNGEGH
}				GMNPSLOAMMLMGFGDIFSMNKAGAVMHSGMQINMQAKQNSSK
1				TTSKRRGKKVNMALGFSDFDLSEGDDDDDDDGEEEYNDMDNSE
99	838	185	328	MLWETGCSAACRVTVSPTVTFATFSTRGIDAMRPGPSFLWRQQ
	030	100		LSQG*
100	839	1	348	PTLGDQPDLHSITRASRPKLCTRKNCNPLTITVHDPNSTQ*YY
===		"		GMSWELRFYIPGFDVGTMFTIQKILVSWSPPKPIGPLTDLGDP
				MFQKPPNKVDLTVPPPFLVIKDTLQKFEKI
101	840	1	416	SLNNVTLPQAKTEKDFIQLCTPGVIKQEKLGTVYCQASSPGAN
			ł	MIGNKMSAISVHGVSTSGGQMYHYDMNTASLSQQ*DQKPIFNV
	<b>†</b>		Ì	IPPIPVGSENWNRCQGSGDDNLTSLGTLNFPGRTVSFSFEMES
1	1			RSVAQAGVQ
102	841	105	354	RHTQECRCPHTHIHTHTHSHTHSHTHSHSHSHTTPRCSHTQPP
	1	1 _	ł	HAQAPALC*S*EDRGQPTWKLCAHRPRLKVIKEGGWLGG
103	842	1.71	347	NYSLSVYLVRQLTAGTLLQKLRAKGIRNPDHSRALSE*HLSSL
}		<u> </u>		PHLIWIQVFLALQPS
104	843	2	690	ATYIVDFGFSTTFREGQMLTAFCGMYPYVAPERSLGQACQ*PA
		İ		RDIQSLSVILYFRNTVGRRARTLPFYS/AEASKLQEKILTGRY
1		)	ł	HAPPLLALQLDSL/IKLLMLNARKCPSL*LMKNPWVKSSQKMP
· ·		İ		LIPYEEPL/RGPPQTIQLMVAMGFQAKNISVAIIERKFNYPMA
		İ		TYLILEHTKQERKCSTIRELSLPPGVPTSPSPSTELSTFPLSL
	J			MRAHREPAFNVQPPEESQ
105	844	2	777	AKQELAKLMRIEDPSLLNSRVLLHHAKAGTIIARQGDQDVSLH FVLWGCLHVYQRMIDKAEDVCLFVAQPGELVGQLAVLTGEPLI
}	1			
	1			FTLRAQRDCTFLRISKSDFYEIMRAQPSVVLSAAHTVAARMSP FVRQMDFAIDWTAVEAGRALYRCSSHRAAQARPRGGDLGVVRP
	1	1		
	1			C*PPRPLRQGDRSDCTYIVLNGRLRSVIQRGSGKKELVGEYGR GDLIGVVSATPTH*PLAFSRPVPRQLTRIIPGNPGSGEVFPGA
	4	<del> </del>	<del> </del>	HASGWTPGTTQTLGQGTAWDTVASTPGTSETTASAEGRRTPGA
106	845	3	709	HASGWTPGTTQTLGQGTAWDTVASTPGTSETTASAEGKRIPGA TRPAAPGTGSWAEGSVKAPAPIPESPPSKSRSMSNTTEGVWEG
	1		[	TRPAAPGTGSWAEGSVKAPAPIPESPPSKSKSMSN1IEGVWEG TRSSVTNRARASKDRREMTTTKADRPREDIEGVRIALDAAKKV
	1			LGTIGPPALVSETLAWEILPQATPVSKQQSQGSIGETTPAAGM
1				WTLGTPAADVWILGTPAADVWTSMEAASGEGSAAGDLDAATGD
	1			RGPQATLSQTPAV*PWGPPG
L				WOLKELINGTING

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
107	846	sequence 3	sequence 406	AGTSGTGDTGPGNTAVSGTPVVSPGATPGAPGSSTPGEADIGN TSFGKSGTPTVSAASTTSSPVSKHTDAASATAVTISGSKPGTP GTPGGATSGGKITPGIA*PTLDQKSPCFSGYGGYFPVNPHQNP CADSL
108	847	1	565	RAHRCCLPLPSLSCEIQIGFS*SSIFPGQ*ACPCSCCRSCRRN WPQSPRCPHHPPAPCSLLLSSCLPPPLSCSWRGTSGKPPSQSP AASRSMRPRCSPRTSSLRGASCRGPGGSAPAAASGPRCRGCSR SPRRCSRSGCAAASPPRSQRRSPPLSPPPFPTSGTLLLKTSRF GSATRE*SSPRPRPRP
109	848		987	DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVADGGV VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSLEVA GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGATGSW RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAAHTS DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATLEDL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPEGGG TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGGWME DYDYVHLTGGRRSF*KTQKELLGKRAA
110	849	84	372	MATDEENVYGLEENAQSRQESTRRLILVGRTGAGKSATGNSIL GQRRFFSRLGATSVTRACTTGSRRWDKCHVEVVDTPDIFSSQV SKTDPGCEERX*
111	850	2	47	TLGLRSLTKEGGGGGDVAAFEVGTGAAASRALGQCGQLQKLIV IFIGSLCGLCTKCAVSNDLTQQEIQTPEIQQRNA*CDSRVTFT NEGGRWWG
112	851	1192	1040	FFFLVETRFHHIGQAGLELLTLSIK*SARLGLPKCWDDRREPP YLAGFMI
113	852	791	362	RRSPPPAPPPLPSPLSPPPRAPVSPASTMPILLFLIDTSASMN QRSHLGTTYLDTAKGAVETFMKLRARDPASRGDRYMLVTFEEP PYAIKAGWKENHATFMNELKNLQAEGLTTLGQSLRTAFDLLNL NRLVTGIDNYGQVG
114	853	812	348	NCRTYVFCFVLVFRLLFLHGSPLSPSLLSRAGLLCGSAENPTP FLCGITMAAGVSLLALVVRVILSTAILCPSGASRRQRSSEVEW GTDSGVYRLYCWRVGFLGPGGELRLGLSEARGGRVWGRGEKRC RVWAVRSLRKGFGSVAALRRGIWAG
115	854	93	170	VTPTPPQYYTCSCVLGFIACSIFLQMSLKPKVMLLTVALVACL VLFNLSQCWQRDCCSQGLGNLTEPSGTNR*GPAAVSWASLPAP SSCR
116	855	1	183	GKAGGAAGLFAKQVQKKFSRAQEK*TRRFGKTCQPEERAREER QEGPEIEFGFSFFSLSLY

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	согге-	corre-	
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
		to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	l	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
l	ĺ	acid	acid	\=possible nucleotide insertion)
1		residue	residue	
Ì	l	of amino	of amino	
	1	acid	acid	•
		sequence	sequence	
117	856	53	2400	PKRLFLFQDVNTLQGGGQPVVTPSVQPSLQPAHPALPQMTSQA
ł	ł	1		PQPSVTGLQAPSAALMQVSSLDSHSAVSGNAQSFQPYAGMQAY
ļ		•	l	AYPQASAVTSQLQPVRPLYPAPLSQPPHFQGSGDMASFLMTEA
]			j	RQHNTEIRMAVSKVADKMDHLMTKVEELQKHSAGNSMLIPSMS
			ł	VTMETSMIMSNIQRIIQENERLKQEILEKSNRIEEQNDKISEL
		]	]	IERNQRYVEQSNLMMEKRNNSLQTATENTQARVLHAEQEKAKV
			]	TEELAAATAQVSHLQLKMTAHQKKETELQMQLTESLKETDLLR
ŀ			)	GQLTKVQAKLSELQETSEQAQSKFKSEKQNRKQLELKVTSLEE
1	1			ELTDLRVEKESLEKNLSERKKKSAQERSQAEEEIDEIRKSYQE
			ł	ELDKLRQLLKKTRVSTDQAAAEQLSLVQAELQTQWEAKCEHLL
1		1	[	ASAKDEHLQQYQEVCAQRDAYQQKLVQLQEKSVCFA\CLALQA
1			l	QITALTKQNEQHIKELEKNKSQMSGVEAAASDPSEKVKKIMNQ
1	1		ł	VFQSLRREFELEESYNGRTILGTIMNTIKMVTLQLLNQQEQEK
1				EESSSEEEEEKAEERPRRPSQEQSASASSGQPQAPLNRERPES
		1	i	PMVPSEOVVEEAVPLPPQALTTSQDGHRRKGDSEAEALSEIKD
Į.	1			GSLPPELSCIPSHRVLGPPTSIPPEPLGPVSMDSECEESLAAS
1	1	}	l	PMAAK\PDNPSGK\VCVQGK*APDGPTYKE\SSTRLFPGFQDP
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118	857	1	791	SETAQQIIDRLRVKLAKEPGANLFLMAVQDIRVGGRQSNASYQ
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		ļ .	1.	LVYDRDTMARLGIDVQAANSLLNNAFGQRQISTIYQPMNQYKV
		1	]	VMEVDPRYTODISALEKMFVINNEGKAIPLSYFAKWQPANAPL
1		ľ	ŀ	SVNHQGLSAALTISFNLPTGKSLSDASAAIDRAMSQLGVPSTV
			] .	RGSFAGPAQVFQETMNSQVILIIAAIATVYIVLGIPYERYVHP
			Ì	PTILL*RPGANLFLMAVODIRVGGROSNASYQYTLLSDDLAAL
1			1	REWEPKIRKKLATLPELADVNSDQQDNGAEMNLVYDRDTMARL
1	1		ĺ	GIDVOAANSLLNNAFGORQISTIYQPMNQYKVVMEVDPRYTQD
1				ISALEKMFVINNEGKAIPLSYFAKWQPANAPLSVNHQGLSAAL
	1		j	TISFNLPTGKSLSDASAAIDRAMSQLGVPSTVRGSFAGPAQVF
[				QETMNSQVILIIAAIATVYIVLGIPYERYVHPPTILL
L	L	<del> </del>	1	
119	858	3	417	IITPDAMGCQKDIAEKIQKQGGDYLFAVKGNQGRLNKAFEEKF
1			1	PLKELNNPEHDSYAISEKSHGREEIRLHIVCDVPDELIDFTFE
		ĺ	[	WKGLKKLCVAVSFRSIIAEQKKEPEMTVRYNIS*LGIAGDISV
L			<u> </u>	TAISGTDD
120	859	2	373	HYLKMLTQARREVIIANAYFFPGYRFLHALRKAARRGVRIKLI
	1	1	1	IQGEPDMPIVRVGARLLYNYLVKGGVQVFEYRRPLHGKVALM
1	ļ	}		DDHWATVGSSNLHPVS*SGNLQANVILHVLRVPTLNP
121	860	286	495	CWSKSAAFHSKLATTCIVPVCAAGHCSAAW*SLRPIEALAKEV
1	1	1	1	RELK*HTR*LLNPATTRELTSLGRNLNRLLKSERERYDKYRTT
	1			LTDLTHSLKTPLAVLQSTLRSLRSEKMSVSDAEPVMLEQISRI
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Or Nucleic Acids         Amino Acids         corresponding to first some in the first samino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence         K = Lysine, L = Leucine, M = Methionine, N = Asparagine, S = Serine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, *= Stop Codon, /= possible nucleotide deletion, l = possible nucleotide insertion)           122         861         2         725         GNTVMFQHLMQKRKHTQWTYGPLTSTLYDLTBIDSSGDEQSLL BLITTYKKREARQILDQTPVKELVSLKWKRYQRPVFCCNLGAYY LLYLICFTMCCIYRPLKPRTNNTSPRDNTLLQKLLQAYWT PKDDIRLVGBLVTVIGAIILLUVEVDDIFRMGVTRFFGQTILG GPFHVLIITYAFMVLVTMVMRLISASGEVVPMSFALVLGWCNV MYFARGFMGLSPTITINGKMIFGDLM           123         862         1         135         EKAAAANIDEVQKSDVSSTGQSVIDKDALGPMMLEVAHLHFSA VF           124         863         2         364         LEVPSEVTPLGFAMQATKTLLLRTCCLQEFNIMEKNKGWALLG GKDGHLQGLFLLANALLERNQLLAQKYMYLLVPLLMRGNDKHK LTAGFFVELLRSPVAKRLPSIYSVARFKDMLQD           125         864         1         374         RPAPAPSAAPSEAPSEP\GVKGRGMAKRKYPAPVMGGAGGGTKS ARRAAAAPDTERSEGGRAVKERYPSSRQPPPSP*PLRCARR CHPNLLAPMPISNBERGKRREEKIRPLSPASTPTSARA           126         865         3         364         LQGVHGSSSTFCSSLSSDFDPLEYCSPKGDPQRVDMQPSVTSR PRSLDSEVPTGETQVSSHVHYHRHRHHYKKRPQRHGKRCPE TGVPQSKRPPSPTPTTQPQPEPPSPDQVTRSNSAAP PRSLDSEVPTGETQVSSHVHYHRHRHHYKKRPQRHGKRPGPE TGVPQSKRPPSPTPTTQPQPEPPSPDQVTRSNSAAP PRSLDSEVPTGETGVDLAFEGGTTSULQRPDTYPSRVS LLLLSFRTCPCKYSFLDNLKKLTRRDVETYPKVR           128         867         194         375		ľ			
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128 867 194 375 AGMSVVVVPPTGSSYLGLISQEHFPNEFTSGDGKKAHQDFGYF YGSSYVAASDSSRTPGL  129 868 104 339 VAAALTLFPQQLSPPGAWGLGLSACFCCAEGFSRLNQQVLSSS LLLLSRTNCPCKYSFLDNLKKLTPRRDVPTYPKVR  130 869 2 360 RDDACLYSPASAPEVITVGATNAQDQPVTLGTLGTNFGRCVDL FAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEP ELTLAELRQRLIHFSAKDVINEAWFPEDQRVLT  131 870 2 105 LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW  132 871 2 466 EAGDADEDEADANSSDCEPEGPVEABEPPQEDSSQSDSVEDR SEDEEDHSEEEETSGSSASEESEESEBAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	127	866	2	250	( · · · · · · · · · · · · · · · · · · ·
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129 868 104 339 VAAALTLFPQQLSPPGAWGLGLSACFCCAEGFSRLNQQVLSSS LLLLSRTNCPCKYSFLDNLKKLTPRRDVPTYPKVR  130 869 2 360 RDDACLYSPASAPEVITVGATNAQDQPVTLGTLGTNFGRCVDL FAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEP ELTLAELRQRLIHFSAKDVINEAWFPEDQRVLT  131 870 2 105 LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW  132 871 2 466 EAGDADEDEADANSSDCEPEGPVEAEEPPQEDSSSQSDSVEDR SEDEEDHSEEEETSGSSASEESEESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	128	867	194	375	
LLLLSRTNCPCKYSFLDNLKKLTPRRDVPTYPKVR  130 869 2 360 RDDACLYSPASAPEVITVGATNAQDQPVTLGTLGTNFGRCVDL FAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEP ELTLAELRQRLIHFSAKDVINEAWFPEDQRVLT  131 870 2 105 LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW  132 871 2 466 EAGDADEDEADANSSDCEPEGPVEAREPPQEDSSSQSDSVEDR SEDEEDEHSEEETSGSSASEESEESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP		-	l	1 222	
RDDACLYSPASAPEVITVGATNAQDQPVTLGTLGTNFGRCVDL   FAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEP   ELTLAELRQRLIHFSAKDVINEAWFPEDQRVLT	129	868	104	339	
FAPGEDIIGASSDCSTCFVSQSGTSQAAAHVAGIAAMMLSAEP ELTLAELRQRLIHFSAKDVINEAWFPEDQRVLT  131 870 2 105 LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW  132 871 2 466 EAGDADEDEADANSSDCEPEGPVEAREPPQEDSSSQSDSVEDR SEDEEDEHSEEETSGSSASEESESEESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP				260	
ELTLAELRQRLIHFSAKDVINEAWFPEDQRVLT  131 870 2 105 LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW  132 871 2 466 EAGDADEDEADANSSDCEPEGPVEAREPPQEDSSSQSDSVEDR SEDEEDEHSEEETSGSSASEESESESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	130	869	2	360	
131 870 2 105 LEIKFLEQVDQFYDDNFPMEIRHLLAQWIENQDW  132 871 2 466 EAGDADEDEADANSSDCEPEGPVEAEEPPQEDSSSQSDSVEDR SEDEEDEHSEEEETSGSSASEESESEESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP		İ			1
132 871 2 466 EAGDADEDEADANSSDCEPEGPVEAEEPPQEDSSSQSDSVEDR SEDEEDEHSEEEETSGSSASEESEESEDAQSQSQADEEEED DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP		<del> </del>	<u> </u>		
SEDEEDEHSEEEETSGSSASEESEESEDAQSQSQADEEEED  DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA  AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG*  135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP					
DDFGVEYLLARDEEQSEADAGSGPPTPGPTTLGPKKEITDIAA AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	132	871	2	466	
AAESLQPKGYTLATTQVKTPIPLLL  133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP				}	
133 872 1 354 LKNLRELLLEDNQLPQIPSGLPESLTELSLIQTNIYNITKEGI SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG*  135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	ļ ·	l	}	ł	
SRLINLKNLYLAWNCYFNKVCEKTNIEDGVFETLTNLELLSLS FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP			<u> </u>	<u> </u>	
FNSLSHVPPKLPSSLRKLFLSNTQIKYISEED  134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG*  135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	133	872	1	354	
134 873 59 184 MRSQALGQSAPSLTASLKELSLPRRGSFPVCPNAGRTSPLG* 135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP	1	1	}		
135 874 1 210 LLCVCLPVGACPSLSLLTAPLNQLMRCLRKYQSRTPSPLLHSV PSEIVFDFEPGPVFRGSWALLSWSTRP			<u> </u>	<u> </u>	
PSEIVFDFEPGPVFRGSWALLSWSTRP	I .				I " " "
	135	874	1	210	l control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
LANC LORE 1491 INEA LORDEVECTONOCINEDES COVERCOCOMISCIONICI MAINTE	L	<u> </u>		<b></b>	
	136	875	131	254	QTPDKKQNDQRNRKRKAEPYETSQGSNNFVSTKVLNSNVLR
	137	876	84	504	YFIIKGMVELVPASDTLRKIQVEYGVTGSFKDKPLAEWLRKYN
					PSEEEYEKASENFIYSCAGCCVATYVLGICDRHNDNIMLRSTG
				1	HMFHIDFGKFLGHAQMFGSFKRDRAPFVLTSDMAYVINGGEKP
TIRFOLFVDL			1	1	I PEDENTERNI.

			<del></del>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
SEQ ID	SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
}	]	to first	to first	T=Inreonine, v=vaine, w=Iryptophan, i=Iytoshie,
ŀ	1	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
•		acid	acid	\=possible nucleotide insertion)
		residue of amino	residue of amino	
		acid	acid	
		sequence	sequence	·
138	877	3	215	PSPLPSLSLPPPVAPGGQESPSPHTAEVESEASPPPARPLPGE
130	• · ·		[	ARLAPISEEGKPOLVGRF\QVTSSK\NRL\$LFPCSQHPPLSLV
}			}	LQNLQPLSSLQRAQIQRTV/PGGGPETREALAESDRAAEGLGA
ł	}		<b>!</b>	GVEEEGDDGKEPQVGGSPQPLSHPSPVWMNYSYSSLCLSSEES
1	1	ĺ	1	ESSGEDEEFWAELQSLRQKHLSEVETLQTLQKKEIEDLYSRLG
1	1	1	1	KQPPPGIVAPAAMLSSRQRRLSKGSFPTSRRNSLQRSEPPGPG
Ì	Ì	i		ETA/GHPASIFSLRPLSVDCFSPGPGGLPRGNRPPLPTSPFLT
1	Ì	ł	}	*CSPSPHTAEVESEASPPPARPLPGEARLAPISEEGKPQLVGR
ł	1			FPSDFIQGTG
139	878	1	337	RRFVSQETGNLYIAKVEKSDVGNYTCVVTNTVTNHKVLGPPTP
			ļ	LILRNDGVMGEYEPKIEVQFPETVPTAKGATVKLECFALGNPV
		ļ		PTIIWRRADGKPIARKARRHKSRVGK
140	879	72	917	MLRTCYVLCSQAGPRSRGWQSLSFDGGAFHLKGTGELTRALLV
1		Í		LRLCAWPPLVTHGLLLQAWSRRLLGSRLSGAFLRASVYGQFVA
1	1	Ì		GETAEEVKGCVQQLRTLSLRPLLAVPTEEEPDSAAKSGEAWYE
	1.	İ		GNLGAMLRCVDLSRGLLEPPSLAEASLMQLKVTALTSTRLCKE
.	Ì	1	1	LASWVRRPGASLELSPERLAEAMDSGQNLQVSCLNAEQNQHLR
ì	1			ASLSRLHRVAQYARAQHVRLLVDAEYTSLNPALSLLVAALAVR
L				WNSPGEGGPWVWNTYQACLKDTF*
141	880	219	308	PHHRIAGDTAIDKNIHQSVSEQIKKNFAK OMTNPFFLCFTTMISNCNFFKGPPGPPGEKGDRGPTGESGPRG
142	881	182	317	~
	1	l	1343	FP NGIIASFFLRTFIFCFIHIQGCQAGQTIKVQVSFDLLSLMFTF
143	882	177	341	VSPCTNDLIH
	1 202	13	1441	VSPCINDBIIH   KLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDTNSTDIA
144	883	3	1441	LKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAV
				AFLYYKSIGPLLSSSDNFLLKPQNYDNSEEEERVISSVISVSM
	1			SSNPPTLYELEKITFTLSHRKVTDRYRSLCAFWNYSPDTMNGS
		1	1	WSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNI
ļ	}	1		LTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCS
1	1			LFLAELVFLVGINTNTNKLFCSIIAGLLHYFFLAAFAWMCIEG
1	1		]	IHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAALGYRY
1	1			YGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFR
1	1	1		HTAGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVVHA
1		1		SVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNVPC
1	1			CFGCLR
145	884	1	429	GTREAAPSRFMFLLFLLTCELAAEVAAEVEKSSDGPGAAQEPT
				WLTDVPAAMEFIAATEVAVIGFFQDLEIPAVPILHSMVQKFPG
	1			VSFGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDIESI
ļ				DATKLSRFIEINSL
146	885	1	156	DETSGLIVREVSIEISRQQVEELFGPEDYWCQCVAWSSAGTTK
1				SRKAYVRIA
147	886	1.	121	GTRSIHVKLDVGKLHTQPKLAAQLRMVDDGSGKVEGLPGI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence 652	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  XCGEDGSFTQVQCHTYTGYCWCVTPDGKPISGSSVQNKTPVCS
148	887			GSVTDKPLSQGNSGRKDDGSKPTPTMETQPVFDGDEITAPTLW IKHLVIKDSKLNNTNIRNSEKVYSCDQERQSALBEAQQNPREG IVIPECAPGGLYKPVQCHQSTGYCWCVLVDTGRPLPGTSTRYV MPSX*
149	888	128	273	VLQLIKSQKFLNKLVILVETEKEKILRKEYVFADSKVSDSKLL KWAVR
150	889	1	948	RRLSLLDLQLGPLGRDPPQECSTFSPTDSGEEPGQLSPGVQFQ RRQNQRRFSMEDVSKRLSLPMDIRLPQEFLQKLQMESPDLPKP LSRMSRRASLSDIGFGKLETYVKLDKLGEGTYATVFKGRSKLT ENLVALKEIRLEHEEGAPCTAIREVSLLKNLKHANIVTLHDLI HTDRSLTLVFEYLDSDLKQYLDHCGNLMSMHNVKVRPRGQGPP ILAATCPEAQCGDPLSPPGIRLLRWLKPSHVGKRERAMPSTSP GTGLSALPQEQTHTVCHCLAVGIKPTLNSEHQFPSLSNGSVSY LPKCREASGEARGYE
151	890	3	108	HERHEPSPTALAFGDHPIVQPKQLSFKIIQVNDN
152	891	2	208	ARGPSLLSEFHPGSDRPQERRTSYEPIHPGPSPVDHDSLESKR PRLEQASDSHYQGHITGESLPGRVH
153	892	1	116	GTRKEEFSAEENFLILTEMATNHVQVLVEFTKKLPGIF
154	893	74	661	HTHKLVAPRPGLPPTSQWPRDAGRQASGGLPSLSTGPPKGPRD GLARGHPAEWLAGSPGNNSPTQGSLPPQLDLYAGALFVHICLG WNFYLSTILTLGITALYTIAGMVPAAGRSTQGTCKGVRRPPPP TGPREQPRKWPQQEPQKFLPVSLLPGARAPSSNLASTGRGPGC CNLHGRPADAHHGGGGCHPDNQR
155	894	55	312	MVNHSLQETSEQNVILQHTLQQQQQMLQQETIRNGELEDTQTK LEKQVSKLEQELQKQRESSAEKLRKMEEKCESAAHEADLKRQK *
156	895	38	185	VCPKWCRFLTMLGHCCYFWHVWPAS*ALSAGPTPTSRSFSPSP LRSIST
157	896	37	462	MRGPPVLLLQAAPMECPVPQGIPAGSSPEPAPDPPGPHFLRQE RSFECRMCGKAFKRSSTLSTHLLIHSDTRPYPCQFCGKRFHQK SDMKKHTYIHTGEKPHKCQTQREPTMVLSPADKTNVKAAWX*
158	897	3	175	HEQLTNNTATAPSATPVFGQVAASTAPSLFGQQTGITASTAVA TPQVISSRFINLDF
159	898	187	677	VSVFKNCPMY*ICIFLTKMFCVLII*NKF*VHKKPLQEVEIA AITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGS ASMASPANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITC IELAERKPPLFNMNAMSALYHIAQNESPTLQSNEW

CEO	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	1	to first	to first	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	1	amino	amino acid	
		acid residue	residue	\=possible nucleotide insertion)
	ł	of amino	of amino	
		acid	acid	
Į		sequence	sequence	
160	899	2	1060	RHARPGGGGHSNQRKMSLEQEEETQPGRLLGRRDAVPAFIEPN
ļ		İ		VRFWITERQSFIRRFLQWTELLDPTNVFISVESIENSRQLLCT
ļ	1	}		NEDVSSPASADQRIQEAWKRSLATVHPDSSNLIPKLFRPAAFL
		ļ	}	PFMAPTVFLSMTPLKGIKSVILPQVFLCAYMAAFNSINGNRSY
				TCKPLERSLLMAGAVASSTFLGVIPQFVQMKYGLTGPWIKRLL
				PVIFLVQASGMNVYMSRSLESIKGIAVMDKEGNVLGHSRIAGT
}		ļ		KAVRETLASRIVLFGTSALIPEVFTYFFKRTQYFRKNPGSLWI
1		ļ		LKLSCTVLAMGLMVPFSFSIFPQIGQIQYCSLEEKIQSPTEET
	1		l	EIFYHRGV
161	900	3	564	HASGRLEVFYNGTWGSVGRRNITTAIAGIVCRQLGCGENGVVS
İ		ł	j	LAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAE
j	ļ	ļ	1	ETWITCEDRIRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAE
		ļ		AEVVCQQLGCGSALAALRDASFGQGTGTIWLDDMRCKGNESFL
ł	<u> </u>			WDCHAKPWGQSDCG
162	901	1099	2	LGDFPQPQRQRRPGASDLPPHLAGARQWEVRFFRHLPARTLPP
		1		SLRMPEGPELHLASQFVNEACRALVFGGCVEKSSVSRNPEVPF
		l l		ESSAYRISASARGKELRLILSPLPGAQPQQEPLALVFRFGMSG
1				SFQLVPREELPRHAHLRFYTAPPGPRLALCFVDIRRFGRWDLG GKWQPGRGPCVLQEYQQFRENVLRNLADKAFDRPICEALLDQR
		<b>J</b>		FFNGIGNYLRAEILYRLKIPPFEKARSVLEALQQHRPSPELTL
			Ì	SQKIRTKLQNPDLLELCHSVPKEVVQLGGRGYGSESGEEDFAA
		}	ļ	FRAWLRCYGMPGMSSLQDRHGRTIWFQGDPGPLAPKGRKSRKK
	1		}	KSKATOLSPEDRVEDALPPSK
163	902	3	335	LTWSACYWRDILRIQLWIAADILLRMLEKALLYSEHQNISNTG
163	302	3	333	LSSQGLLIFAELIPAIKRTLARLLVIIASLDYGIEKPHLGTGM
1	1			HRVIGLMLLYLIFANAESVIRVIG
164	903	12	135	FFFEMESRSAAQAGVQWCNLGSLQALPPRFTPFSCLSLPSSWD
104	1 303	1	133	Y
165	904	74	645	YECEELAKKLENSQRDGISRNKLALAELYEDEVKCKSSKSNRP
100		-		KATVFKSPRTPPQRFYSSEHEYSGLNIVRPSTGKIVNELFKEA
}			1	REHGAVPLNEATRASGDDKSKSFTGGGYRLGSSFCKRSEYIYG
	1		1	ENQLQDVQILLKLWSNGFSLDDGELRPYNEPTNAQFLESVKRG
				VTLIACMPEIQQLMLEIF
166	905	14	1257	WPCGAAPGLTHASERMFTLTTMIQALAPVMGWDRKPLKMFSSE
				EMRGHLHHHHKCLTKILKVEGQVPDLPSCLPLTDNTRMLASIL
1			1	INMLYDDLRCDPERDHFRKICEEYITGKFDPQDMDKNLNAIQT
1				VSGILQGPFDLGNQLLGLKGVMEMMVALCGSERETDQLVAVEA
1	1	Ì	1	LIHASTKLSRATFIITNGVSLLKQIYKTTKNEKIKIRTLVGLC
1	1			KLGSAGGTDYGLRQFAEGSTEKLAKQCRKWLCNMSIDTRTRRW
-	1			AVEGLAYLTLDADVKDDFVQDVPALQAMFELAKTSDKTILYSV
-	1	1		ATTLVNCTNSYDVKEVIPELVQLAKFSKQHVPEEHPKDKKDFI
ļ	1	I	1	DMRVKRLLKAGVISALACMVKADSAILTDQTKELLARVFLALC
1	1	1	1	DNPKDRGTIVAQGGGKALIPLALEGTD

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
Ì	ļ	to first	to first	1 = inreonnie, v = vainie, w = iryptophan, i - rytosnie,
	ļ	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	ļ	acid residue	acid residue	\=possible nucleotide insertion)
		of amino	of amino	
<u> </u>		acid	acid	
[		sequence	sequence	
167	906	3	894	VDSVGGGSESRSLDSPTSSPGAGTRQLVKASSTGTESSDDFEE
				RDPDLGDGLENGLGSPFGKWTLSSAAQTHQLRRLRGPAKCREC
ĺ	İ	[		EAFMVSGTECEECFLTCHKRCLETLLILCGHRRLPARTPLFGV
i	l	İ		DFLQLPRDFPEEVPFVVTKCTAEIEHRALDVQGIYRVSGSRVR
			ł	VERLCQAFENGRALVELSGNSPHDVSSVLKRFLQELTEPVIPF
		}		HLYDAFISLAKTLHADPGDDPGTPSPSPEVIRSLKTLLVQLPD
Į		}	l	SNYNTLRHLVAHLFRVAARFMENKMSANNLGIVFGPTL
168	907	1	394	GLHVISLHSADGRHWEDPLSELDSERVSAFLVTETLVFYLFCL
ļ	Ì	ļ		LADETVVPPDVPSYLSSQGTLSDRQETVVRTEGGPQANGHIES
ļ	]	]		NGKASVTVKQSSAVTVSLGAGGGLQVFTGQVPGIRWGKLGEAH
1	İ	]		AS
169	908	179	551	KIKHRPEEEPRWAAAGAQSAGPGAAEVAPPRPGTVAPGANGMT
	1			DSATANGDDRDPEIELFVKAGIDGESIGNCPFSQRLFMILWLK
	ł		1	GVVFNVTTVDLKRKPADLRNLAPGTHPPFLAFNWYVKT
170	909	1	335	LGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYIGRKKI
ļ	1			SPPTPKPRPPRPLPVAPGSSKTEADVEQQVLYKYRKKPSSSHR
	1		L	PQTPHNGKSKNFLHKQGLKKKKASL
171	910	1	895	RTRGVMELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKE
}	1	j		VWDYVTVRKDAYMFWWLYYATNSCKNFSELPLVMWLQGGPGGS
}	İ	] .		STGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
<b>\</b>	1	İ		VNGSGAYAKDLAMVASDMMGLLKTFFSCHKEFQTVPFYIFSES
1				YGGKMAAGIGLELYKAIQRGTIKCNFAGVALGDSWISPVDSVL
1		l .		SWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYREATELW
				GKAEMIIEQVKRGNTQRRACLAFSGGYRAHGWCCQTWSLH
172	911	553	194	PGWSRSPDLVIRLPRPPKVLGLQYYHFFFFLRWSL/DSVAQAE
		1.		VQWHDLRSLQAPPPGFTPFSCLSLPGSWDYRCPPPRPANFLYF
İ		1		**RRGFTVLARMVSIS*PRDPPASASQSAGITVLSLFFFFEME SCSVAQAGVQWRYLGSLQALPPGFTPFSCLSLPSSWDYRRPPP
	1	1		RPANFFVFLVETGVSPC*PGWSRSPDLVIRLPQPPKVLGLQV
<u></u>	<u> </u>	1.50	<del>  _ ` _ </del>	PSMKTGELEKETAPLRKDADSSISVLEIHSQKAQIEEPDPPEM
173	912	1761	1	ETSLDSSEMAKDLSSKTALSSTESCTMKGEEKSPKTKKDKRPP
1	1	1		ILECLEKLEKSKKTFLDKDAORLSPIPEEVPKSTLESEKPGSP
			<b> </b>	EAAETSPPSNIIDHCEKLASEKEVVECOSTSTVGGQSVKKVDL
	İ			ETLKEDSEFTKVEMDNLDNAQTSGIEEPSETKGSMQKSKFKYK
1			ì	LVPEEETTASENTEITSERQKEGIKLTIRISSRKKKPDSPPKV
			1	LEPENKQEKTEKEEEKTNVGRTLRRSPRISRPTAKVAEIRDQK
			1	ADKKRGEGEDEVEEESTALQKTDKKEILKKSEKDTNSKVSKVK
{	1	}		PKGKVRWTGSRTRGRWKYSSNDESEGSGSEKSSAASEEEEEKE
1	1	1	1	SEEAILADDDEPCKKCGLPNHPELILLCDSCDSGYHTALPFAP
	1			PLMIHPQMGGW\F\CPTFCPTLNLLLLEKLEDQF\QDL\DVAL
	}			KKERALPERRK\ERLVYVGI\SIENIIPPQ\EPDFSEDQEEKK
	}			KDSKKSKANLL\ERRSTRTRKCISYRFDEFDEAIDEAIEDDIK
1				EADGGGVGRGKDISTITGHRGKDISTILDEER
L	L	J	1	HADGGG AGEGID TO LEIGHBURK

SEQ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of Nucleic	of Amino	corre-	согге-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acius	Acias	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	i	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	1	acid	acid	\=possible nucleotide insertion)
	]	residue	residue	
	İ	of amino	of amino	
		acid	acid	,
		sequence	sequence	
174	913	3	539	KRRGSFKMAELDQLPDESSSAKALVSLKEGSLSNTWNEKYSSL
		1		QKTPVWKGRNTSSAVEMPFRNSKRSRLFSDEDDRQINTRSPKR
	ļ	ļ.	}	NORVAMVPQKFTATMSTPDKKASQKIGFRLRNLLKLPKAHKWC
	ļ	<b>,</b>	}	IYEWFYSNIDKPLFEGDNDFCVCLKESFPNLKTRKLTRVEWGK
			l	IRRLMG
175	914	166	635	MPEYLRKRFGGIRIPIILAVLYLFIYIFTKISVDMYAGAIFIQ
	ļ			QSLHLDLYLAIVGLLAITAVYTVAGGLAAVIYTDALQTLIMLI
	}	1	l	GALTLMGYSFAAVGGMEGLKEKYFLALASNRSENSSCGLPRED
				AFHIFRDPLTSDLPWPGVLFGMSIPSLX*
176	915	673	1025	XSASATSLTLSHCVDVVKGLLDFKKRRGHSIGGAPEQRYQIIP
	]			VMCCSLLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVD
	,		l	FDPSGYQVLAATYNQVAQFWK*
177	916	3	139	QKRFPSNCGRDGKLFLWGQALHIIAKLLGKWRRLGMVFFSLLL
		(	1	SY
178	917	1	541	VHVCSSKMGALSTERLQYYTQELGVRERSGHSVSLIDLWGLLV
	l		1	EYLLYQEENPAKLSDQQEAVRQGQNPYPIYTSVNVRTNLSGED
		}	ļ	FAEWCEFTPYEVGFPKYGAYVPTELFGSELFMGRLLQLQPEPR
		ļ	ļ	ICYLQGMWGSAFATSLDEIFLKTAGSGLSFLEWYRGSVNITDD
		ļ	İ	COKPOLHN
179	918	1	628	EFLGRPTRPAKDEGNDEGKDEGKDEGKDEGKDEGKDERK
1		<b>\</b>	<b>[</b>	DEGKDEGKDEGKDEGKDEGKDEGKDEGKDEGKDEGKDEG
1	1	-		NDEGKDEGKDEGKDEGKDEGKDERKDE
		ļ		GKDEGKDEGKDEGKDEGKDEGKDEGKDEGKD
	1	ł		EGKDEGKDEGNDEGNDEGNDEGKDEGKDEGKDEGK
	1	1	į.	DEGKDEGKDERNDEGKDERKDEGKDEGKDEGKDEGKDEG
	ļ			NDEGKDERKDEGKDEGKDK
180	919	27	471	PSLRPAWHEGEDFSYGLQPYCGYSFQVVGEMIRNREVLPCPDD
1	1			CPAWAYALMIEGWNEFPSRRARFKDIHSRLRAWGNLSNYNSSE
	ì		İ	QTSGGRNTTQTSSLSTSPLCNVSNAPYVGPKQKVPPFPQTQVI
ĺ	_		İ	PMKGQIRPMVPPPQLYVP
181	920	2	454	RNSGRHPRVRWILEERKRVMQEACAKYRASSSRRAVTPRHVSR
				IFVEDRHRVLYCEVPKAGCSNWKRVLMVLAGLASSTADIQHNT
1	1		1.	VHYGSALKRLDTFDRQGILHRLSTYTKMLFVREPFERLVSAFR
	L_	l		DKFEHPNSYYHPVFCMAILAR
182	921	2	378	IMYSISPANSEEGQELYVCTVKDDVNLDTVLLLPFLKEIAVSQ
1	1 .		ł	LDQLSPEEQLLVKCAAIIGHSFHIDLLQHLLPGWDKNKLLQVL
1	1	1		RALVDIHVLCWSDKSQELPAEPILMPSSIDIIDGTKEKK
183	922	181	513	GPHVVLVLRRCFLLSYFKGVEKAKAMPSPRILKTHLSTQLLPP
	1			SFWENNCKVRYQQLPVTEGKVSQPKRVLQTPTQSIRDHLCLST
			Ì	VSDAYQQRENIKFYIQQDIHLNSFK
184	923	32	239	FYYICRLSKEDKAFLWEKRYYCFKHPNCLPKILASAPNWKWVN
				LAKTYSLLHQWPALYPLIALELLDSK
1		_1	1	<u></u>



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide insertion)
		sequence	sequence	THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
185	924	3	361	KMMI*GLFEIQQCPIGKHCNFLQVLRN/PNRDL/WLVSSFGKS SKGRERMGHHDEYYRLRGR/HNPSPDHSYKRNGESERKRKKSH *HMSKSQERHNSPSRGRNSDRSGGRCSRSDNGRSRYR
186	925	443	1412	PLSLFARVAGSRVEMPEPPGLGDEGRPLLHPGRREAVGSWVSA FAGDSTPCGPGDLSVPRREPFRLTAL*PHRSPVVRTSLIGLLL GFSVKEELRGVGWAARTPLGIR
187	926	2	917	FDKRQHEARIQQMENEIHYLQENLKSMEEIQGLTDLQLQEADE EKERILAQLRELEKKKKLEDAKSQEQVFGLDKELKKLKKAVAT SDKLATAELTIAKDQLKSLHGTVMKINQERAEELQEAERFSRK AAQAARDLTRAEAEIELLQNLLRQKGEQFRLEMEKTGVGTGAN SQVLEIEKLNETMERQRTEIARLQNVLYLTGSDNKGGFENVLE EIAELRREGSYQNDYISSMADPFKRRGYWYFMPPPPSSKVSSH SSQATKDSGVGLKYSASTPVRKPRPGQQDGKEGSQPPPASGYW VYSP
188	927	171	1082	SDASSFKTRVIVVPRPRVFPLGSAITENSLESDSQIGQFGVGF YSAFLVADKVIVTSKHNNDTQHIWESDSNEFSVIADPRGNTLG RGTTITLVLKEEASDYLELDTIKNLVKKYSQFINFPIYVWSSK TETVEEPMEEEEAAKEEKEESDDEAAVEEEEEKKPKTKKVEK TVWDWELMNDIKPIWQRPSKEVEEDEYKAFYKSFSKESDDPMA YIHFTAEGEVTFKSILFVPTSAPRGLFDEYGSKKSDYIKLYVR RVFITDDFHDMMPKYLNFVKGVVDSDDLPLNVSRETLQQHKLL KV
189	928	718	275	CGSWMRRALIPPCRGGPSASDRCCSCSPSGFSAGRGRCPVQGC LRPHRVQLLRRWGPGSPAGQRLSKGFQLLRWWGPGSPAPEPRK GPFPPPDPPWPVTAVTVMAGSVPSAQSVDALESPGPLALEGPS SPRNLLWREMSIFLPGIF
190	929	1	550	PGPTPPPRHGSPPHRLIRVETPGPPAPPADERISGPPASSDRL AILEDYADPFDVQETGEGSAGASGAPEKVPENDGYMEPYEAQK MMAEIRGSKETATQPLPLYDTPYEPEEDGATPEGEGAPWPRES RLPEDDERPPEEYDQPWEWKKERISKAFAVDIKVIKDLPWPPP VGQLDSSPSLP
191	930	1	562	QFFSLFLRYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVG YSTHMVGKWHLGFYRKECMPTRRGFDTFFGSLLGSGDYYTHYK CDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQILASHN PTKPIFLYIAYQAVHSPLQAPGRYFEHYRSIININRRRYAAML SCLDEAINNVTLALK
192	931	3	580	RVRKGRGGERLQSPLRVPQKPERPPLPPKPQFLNSGAYPQKPL RNQGVVRTLSSSAQEDIIRWFKEEQLPLRAGYQKTSDTIAPWF HGILTLKKANELLLSTGMPGSFLIRVSERIKGYALSYLSEDGC KHFLIDASADAYSFLGVDQLQHATLADLVEYHKEEPITSLGKE LLLYPCGQQDQLPDYLELFE

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
l	[	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	·	acid	acid	\=possible nucleotide insertion)
(	ŀ	residue	residue	/=possible indefeddae insertion/
1	]	of amino	of amino	
	1	acid	acid	<b>.</b> .
1	į	sequence	sequence	
193	932	3	1641	GSLEKALFQLLKVWGQWAEQTRRLQRLDVSLSVARVRSAGPSC
1 2 3		-	1	ONKGDLVMEALLEGIQNRGHGGGFLTSCEAELQELMKQIDIMV
	İ			AHKKSEWEGRTHALETCLKIREQELKSLRSQLDVTHKEVGMLH
İ	Ĭ	1	ļ	QQVEEHEKIKQEMTMEYKQELKKLHEELCILKRSYEKLQKKQM
}	ļ		}	REFRGNTKNHREDRSEIERLTAKIEEFRQKSLDWEKQRLIYQQ
l	ļ	j	1	QVSSLEAQRKALAEQSEIIQAQLVNRKQKLESVELSSQSEIQH
1	ł	}		LSSKLERANDTICANELEIERLTMRVNDLVGTSMTVLQEQQQK
	1	1	ŀ	EEKLRESEKLLEALQEEKRELKAALQSQENLIHEARIQKEKLQ
l	[	İ	į	EKVKATNTQHAVEAISLESVSATCKQLSQELMEKYEELKRMEA
1	1	1	J	HNNEYKAEIKKLKEQILQGEQSYSSALEGMKMEISHLTQELHQ
1	İ		ł	RDITIASTKGSSSDMEKRLRAEMQKAEDKAVEHKEILDQLESL
}	]	)	j	KLENRHLSEMVMKLELGLHECSLPVSPLGSIATRFLEEEELRS
1		1	ł	HHILERLDAHIEELKRESEKTVRQFTALK
L	ļ		<del>  </del>	TGFLGWSQGPSLTPTSLSALYPSQVEETGVVLSLEQTEQHSRR
194	933	159	1053	PIQRGAPSQKDTPNPGDSLDTPGPRILAFLHPPSLSEAALAAD
1	1	1	1	PRRFCSPDLRRLLGPILDGASVAATPSTPLATRHPQSPLSADL
1	]		1	PDELPVGTENVHRLFTSGKDTEAVETDLDIAQDADALDLEMLA
1 .	1		1	
1	1		1	PYISMDDDFQLNASEQLPRAYHRPLGAVPRPRARSFHGLSPPA
]		1		LEPSLLPRWGSDPRLSCSSPSRGDPSASSPMAGARKRTLAQSS
1	l	<u> </u>	L	KDEDEGVELLGVRPPKRSPSPEHENFLLFPLSLSFLLTG
195	934	3	425	ELQDCFDVHDASWEEQIFWGWHNDVHIFDTKTQTWFQPEIKGG
1		1	İ	VPPQPRAAHTCAVLGNKGYIFGGRVLQTRMNDLHYLNLDTWTW
	}	1	ļ	SGRITINGESPKHRSWHTLTPIADDKLFLCGGLNAYNMPLSDG
		ľ	1	WIHNVTTHCWK
196	935	2	295	FFFLRTRSHSVTPRWECSDDITAHWQPQPWGSSDPLTFS/RPQ
		}	}	VVVPPRHTTLCP\ANFFVFCIFCRNRISPCWPGWSRTPWAQLI
1		1	1	RLPRPPKVLGLQV
197	936	2	737	PREGQVKQGLLGDCWFLCACAALQKSRHLLDQVIPPGQPSWAD
			1	QEYRGSFTCRIWQFGRWVEVTTDDRLPCLAGRLCFSRCQREDV
1	l		1	FWLPLLEKVYAKVHGSYEHLWAGQVADALVDLTGGLAERWNLK
ł	1		1	GVAGSGGQQDRPGRWEHRTCRQLLHLKDQCLISCCVLSPRAGE
1	1	1	1	ARGOHGRAAASVPPTARPOAHCSFLCDWLHSPVRTKWEEVSLF
1	1		j	SRVVSSVCDLPLLSSSRGTWPFSPLTSPFH
198	937	- 3	638	AECLEAS IARYAHRVANSRYTFDGETVTLSPSQGVNQLHGGPE
1 200	1 -3.	1		GFDKRRWQIVNQNDRQVLFALSSDDGDQGFPGNLGATVQYRLT
1	1		1	DDNRISITYRATVDKPCPVNMTNHVYFNLDGEQSDVRNHKLQI
1	1			LADEYLPVDEGGIPHDGLKSVAGTSFDFRSAKIIASEFLADDD
				QRKVKGYDHAFLLQAKGDGKKVAAHVWSADEKLQLKVYT
	1-026		425	PLSRFLSKESQEDWGMERQSRVMSEKDEYQFQHQGAVELLVFN
199	938	69	445	FLLILTILTIWLFKNHRFRFLHETGGAMVYDKPPKFAMSREQM
	1			SQSCSHTAHNASLLTDAGPLSCGESRASCLFL
	1	1	1	SQSCSHTAHNASILLTDAGFLSCGESKASCUFL



		Duration d	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	Predicted beginning	end end	Amino acid segment containing signal peptide (A—Alainine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of Nuclais	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic Acids	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	, possion number 1,
	ļ	of amino	of amino	
	ļ	acid	acid	
	1	sequence	sequence	
200	939	3	435	DSKEPRLQQLGLLEEEQLRGLGFRQTRGYKSLAGCLGHGPLVL
-	1	1	1	QLLSFTLLAGLLVQVSKVPSSISQEQSRQQAIYQNLTQLKAAV
	ļ	l	}	GELSEKSKLQEIYQELTQLKAAVGELPEKSKLQEIYQELTWLK
ł	1	į		AAVGELPEKSKMQE
201	940	657	469	MQSIAWGHRRDRGESPLGWGQESEASPSALTEAPKAAHTTRLG
			1	FLAANNPNGHSQPQDSFLL*
202	941	1	714	FETLSMRGIPHMLALGPQQLLAQDEEGDTLLHLFAARGLRWAA
		] _		YAAAEVLQVYRRLDIREHKGKTPLLVAAAANQPLIVEDLLNLG
	ļ	1		AEPNAADHQGRSVLHVAATYGLPGVLLAVLNSGVQVDLEARDF
ļ	ļ	]	ļ	EGLTPLHTAILALNVAMRPSDLCPRVLSTQARDRLDCVHMLLQ
		1	1	MGANHTIQVSGDVGGQTLGDCVEWGHLDVRELQANADFASSLL
		1		RALEHVTSLLCALRVFCLFLCQL
203	942	3	479	DAWADAWVGTKMADLDSPPKLSGVQQPSEGVGGGRCSEISAEL
203	342	3	13,75	IRSLTELQELEAVYERLCGEEKVVERELDALLEQONTIESKMV
ĺ		1	j	TLHRMGPNLQLIEGDAKQLAGMITFTCNLAENVSSKVRQLDLA
ĺ	İ	i	1	KNRLYQAIQRADDILDLKFCMDGVQTALR
004	943	1	706	AVEFRVPRSGSAYLYSYVTVGELWAFTTGWNLILSYVIGTASV
204	943	1 *	/08	ARAWSSAFDNLIGNHISKTLQGSIALHVPHVLAEYPDFFALGL
1	1		1	VLLLTGLLALGASESALVTKVFTGVNLLVLGFVMISGFVKGDV
	1	1		HNWKLTEEDYELAMAELNDTYSLGPLGSGGFVPFGFEGILRGA
1		1	1	ATCFYAFVGFDCIATTGEEAQNPQRSIPMGIGISLSVCFLADF
ł		ŀ	1	AVSSALTLMMPYYQLQPESP
	<u> </u>	ļ <u>_</u>	<del> </del>	GFHPNTTHYRARAARAGAGSFVGEVSAVDKDFGPNGEVRYSF
205	944	1	852	EMVQPDFELHAISGEITNTHQFDRESLMRRRGTAVFSFTVIAT
	1.			DQGIPQPLKDQATVHVYMKDINDNAPKFLKDFYQATISESAAN
	}		1	LTOVLRVSASDVDEGNNGLIHYSIIKGNEERQFAIDSTSGQVT
İ	}	1	1	LIGKLDYEATPAYSLVIQAVDSGTIPLNSTCTLNIDILDENDN
j	}	}	1	TPFF/LLNQHFFVDVLENMRIGELGASGTATDS\DSGDIADLY
1	ļ	1	ŀ	
		<u> </u>		YKFTGTKHPPGTFSISPKHLGVFFLAQK
206	945	3	363	GDCYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKNPL
	[	1		NCADPTSQRWFHGHLSGKEAEKLLTEKGKHSSFLVRESQSHPG
	1			DFVLSVCTGDDKGESNDGKSKVTHVMIHCQELK
207	946	218	717	IDSGNQNGGNDDKTKNAERNYLNVLPGEFYITRHSNLSEIHVA
1		1		FHLCVDDHVKSGNITARDPAIMGLRNILKVCCTHDITTISIPL
1			1	LLVHDMSEEMTIPWCLRRAELVFKCVKGFMMEMASWDGGISRT
1				VQFLVPQSISEEMFYQLSNMLPQIFRVSSTLTLTSKH
208	947	3	368	SILPALLVTILIFMDQQITAVIVNRKENKLKKAAGYHLDLFWV
	1			GILMALCSFMGLPWYVAATVISIAHIDSLKMETETSAPGEQPQ
1	1		1	FLGVREQRVTGIIVFILTGISVFLAPILKCIPLPV
209	948	2	575	GASRVEAGSANGMLIDGGSQIVKVQGHADGTTINKSGSQDVVQ
	1		1	GSLATNTTINGGRQYVEQSTVETTTIKNGGEQRVYESRALDTT
}	1			IEGGTOSLNSKSTAKNTHIYSGGTQIVDNTSTSDVIEVYSGGV
	1			LDVRGGTATNVTQHDGAILKTNTNGTTVSGTNSEGAFSIHNHV
	1			ADNVLLENGGHLDINAYGS
			ــــــــــــــــــــــــــــــــــــــ	<u></u>



000	GEO	Deadistad	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	Predicted beginning	end	Amino acid segment containing signal peptide (A=Alainine,
ID	ID NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO: of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	согте-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
110.00	Acids .	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	1	acid	acid	\=possible nucleotide insertion)
		residue	residue	
l	j	of amino	of amino	
		acid	acid	,
		sequence	sequence	FFSSIQLTDDQGPVLMTTVAMPVFSKQNETRSKGILLGVVGTD
210	949	1	296	1
				VPVKELLKTIPKYKVMNDLIPEIKATEMPRALFSQSSGFKLYF
				GAMFLLTTITAC
211	950	3	594	SCSGTGTNACYMEDMSNIDLVEGDEGRMCINTEWGAFGDDGAL
		ĺ	1	EDIRTEFDRELDLGSLNPGKQLFEKMISGLYLGELVRLILLKM
			ł	AKAGLLFGGEKSSALHTKGKIETRHVAAMEKYKEGLANTREIL
		ļ	,	VDLGLEPSEADCIAVQHVCTIVSFRSANLCAAALAAILTRLRE
		Í		NKKVERLRTTVGMDGTLYKIHPQY
212	951	2	2167	FVAIATNGVVPAGGSYYMISRSLGPEFGGAVGLCFYLGTTFAG
}	1	ł	ł	AMYILGTIEILLAYLFPAMAIFKAEDASGEAAAMLNNMRVYGT
[	{		[	CVLTCMATVVFVGVKYVNKFALVFLGCVILSILAIYAGVIKSA
l	}	1	1	FDPPNFPICLLGNRTLSRHGFDVCAKLAWEGNETVTTRLWGLF
	1	j		CSSRFLNATCDEYFTRNNVTEIQGIPGAASGLIKENLWSSYLT
1	1	1		KGVIVERSGMTSVGLADGTPIDMDHPYVFSDMTSYFTLLVGIY
į	1	j	Į.	FPSVTGIMAGSNRSGDLRDAQKSIPTGTILAIATTSAVYISSV
ļ		ł		VLFGACIEGVVLRDKFGEAVNGNLVVGTLAWPSPWVIVIGSFF
.		1		STCGAGLQSLTGAPRLLQAISRDGIVPFLQVFGHGKANGEPTW
1	}	ł	l	ALLLTACICEIGILIASLDEVAPILSMFFLMCYMFVNLACAVQ
	1		[	TLLRTPNWRPRFRYYHWTLSFLGMSLCLALMFICSWYYALVAM
	1	1	1	LIAGLIYKYIEYRGAKKEWGDGIRGLSLSAARYALLRLEEGPP
	Ì	1		HTKNWRPQLLVLVRVDQDQNVVHPQLLSLTSQLKAGKGLTIVG
		İ		SVLEGTFLENHPQAQRAEESIRRLMEAEKVKGFCQVVISSNLR
{		1	1	DGVSHLIQSGGLGGLQHNTVLVGWPRNWRQKEDHQTWRNFIEL
		ļ	}	VRETTAGHLALLVTKNVSMFPGNPERFSEGSIDRWGIGHDGGM
	<u> </u>			LMLVPFLLRHHKVWRKCKMRIFTVAQMVDMHAM
213	952	1	128	FYLRLLSFFCFQEHEKRCWSVDFNLMDPKLLASGSDDAKGTV
214	953	3	244	RNSKAMHRSSCDGPLLSLPSVGRSATHALVQAQLICSGARRGM
				HAFIVPIRSLQDHTPLPGKPIMLPQGTLPGGEPRWPP
215	954	2	609	CGTLILQARAYVGPHVLAVVTRTGFCTAKGGLVSSILHPRPIN
ì			ł	FKFYKHSMKFVAALSVLALLGTIYSIFILYRNRVPLNEIVIRA
				LDLVTVVVPPALPAAMTVCTLYAQSRLRRQGIFCIHPLRINLG
1		1	ľ	GKLQLVCFDKTGTLTEDGLDVMGVVPLKGQAFLPLVPEPRRLP
			<u> </u>	VGPLLRALATCHALSRLQDTPVGDPMDLKM
216	955	292	855	QIEYFRSLLDEHHISYVIDEDVKSGRYMELEQRYMDLAENARF
	ĺ		1	EREQLLGVQQHLSNTLKMAEQDNKEAQEMIGALKERSHHMERI
	J			IESEQKGKAALAATLEEYKATVASDQIEMNRLKAQLENEKQKV
1	1			AELYSIHNSGDKSDIQDLLESVRLDKEKAETLASSLQEDLAHT
	1		<u> </u>	RNDANRLQDAIAKGRG
217	956	2	400	ARYRFTLSARTQVGSGEAVTEESPAPPNEATPTAAPPTLPPTT
1				VGATGAVSSTDATAIAATTEATTVPIIPTVAPTTMATTTTVAT
1	1			TTTTTAAATTTTESPPTTTSGTKIHESAPDEQSIWNVTVLPNS
]	1	1	<u> </u>	KWA
<del></del>			<del></del>	<u> </u>

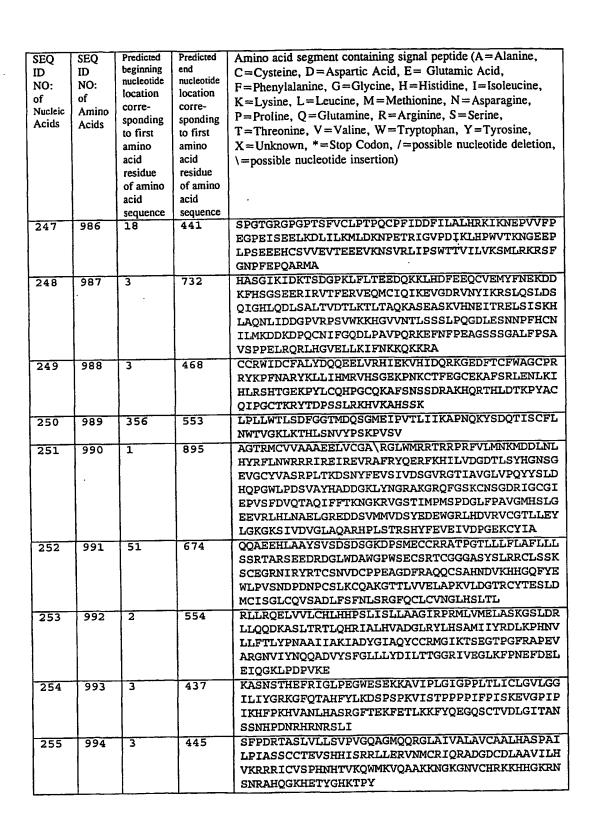


		<b>7</b>	Dunding	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	}	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
ļ	1	residue	residue	1—possible nucleotide insertiony
		of amino	of amino	
1	1	acid	acid	
		sequence	sequence	
218	957	1	662	LKSTQDEINQARSKLSQLHESRQEAHRSLEQYDQVLDGAHGAS
		-	1	LTDLANLSEGVSLAERGSFGAMDDPFKNKALLFSNNTQELHPD
1		1	!	PFQTEDPFKSDPFKGADPFKGDPFQNDPFAEQQTTSTDPFGGD
	1			PFKESDPFRGSATDDFFKKQTKNDPFTSDPFTKNPSLPSKLDP
	ł			FESSDPFSSSSVSSKGSDPFGTLDPFGSGSFNSAEGFADFSTI
Ì	l			EGRRG
219	958	1	752	RTRGGSGNSSQPSLREGHDKPVFNGAGKPHSSTSSPSVPKTSA
ودء		-	, 52	SRTOKSAVEHKAKKSLSHPSHSRPGPMVTPHNKAKSPGVRQPG
1	J		]	SSSSSAPGQPSTGVARPTVSSGPVPRRQNGSSSSGPERSISGS
1		1		KKPTNDSNPSRRTVSGTCGPGQPASSSGGPGRPISGSVSSARP
		1		LGSSRGPGRPVSSPHELRRPVSGLGPPGRSVSGPGRSISGSIP
1				AGRTVSNSVPGRPVSSLGPGQTVSSSGPTIKPKCT
	050	439	582	RGKGITPRYHLCISDPHNLKICCRVNGEVVQSSNTNQMVFKTE
220	959	439	362	DLIAW
		<u> </u>	400	VVAVTRWLCENGVSYLRKCVCSACRHGTRCAGEVAAAANNSHC
221	960	230	420	1 17
				TVGIAFNAKIGGMGNQLTWM GAPPPFVPTLKSDDDTSNFDEPKKNSWVSSSPCQLSPSGFSGE
222	961	311	490	1
		<u> </u>	<del> </del>	ELPFVGFSYSKALGIL FVERLAHLHAACAPRRKVALLLEVCRDVYAGLARGENQDPLGA
223	962	2	422	DAFLPALTEELIWSPDIGDTQLDVEFLMELLDPDELRGEAGYY
				LTTWFGALHHIAHYQPETDRAPRGLSSEARASLHQWHRRRTLH
	1			
			<del> </del>	RKDHPRAQQLD FWMDPYNPLNFKAPFQTSGENEKGCRDSKTPSESIVAISECHT
224	963	385	844	LLSCKVQLLGSQESECPDSVQRDVLSGGRHTHVKRKKVTFLEE
		i	ı	VTEYYISGDEDRKGPWEEFARDGCRFQKRIQETEDAIGYCLTF
		<u> </u>		EHRERMFNRLQGTCFKGLNVLKQC
225	964	3	166	AASTAYSFFGTVENMAPKVVNRPGHTQSADWGSFGGLMGRFEF
	L			GIFLKGKEIVK
226	965	1	118	GFVFLPGPMSVGLDFSLPGMEHVYGIPEHADNLRLKVTE
227	966	1	390	GSECQGTDLDTRNCTSDLCVHTASGPEDVALYVGLIAVAVCLV
j	1	}		LLLLVLILVYCRKKEGLDSDVADSSILTSGFQPVSIKPSKADN
1				PHLLTIQPDLSTTTTTYQGSLCPRQDGPSPKFQLTNGHLLSPL
	L			G
228	967	1	777	LIYNEDMICWIESRESSNQLKCIQITKAGGLTDEWTINILQSF
İ				HNVQQMAIDWLTRNLYFVDHVGDRIFVCNSNGSVCVTLIDLEL
				HNPKAIAVDPIAGKLFFTDYGNVAKVERCDMDGMNRTRIIDSK
1				TEQPAALALDLVNKLVYWVDLYLDYVGVVDYQGKNRHAVIQGR
1				QVRHLYGITVFEDYLYATNSDSYNIVRISRFNGTDIHSLIKIE
1				NAWGIRIYQKRTQPTVRSHACEVDPYGMPGGCSHICLLSSSYT
1				K
229	968	3	488	SSGNPQPGDSSGGGAGGGLPSPGEQELSRRLQRLYPAVNQQET
				PLPRSWSPKDKYNYIGLSQGNLRVHYKGHGKNHKDAASVRATH
		[		PIPAACGIYYFEVKIVSKGRDGYMGIGLSAQGVNMNRLPGWDK
	1			HSYGYHGDDGHSFCSSGTGQPYGPTFTTGDVI
L				_l

SEQ	SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	согге-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	\=possible nucleotide insertion/
		of amino	of amino	
		acid	acid	,
		sequence	sequence	
230	969	1	228	FFFFKMGSRSVTQAGVQWCDVSSLQAPPPRFTLFCLSLPSSWD
230	969	*	220	YRCVPPCPANFFVFLVETGFHRVSQYGLDLLTS
231	970	2	119	QLSLARGKVFLCALSFVYFAKALAEGYLKSTITQIERRVDIPS
	1	1		SLVGVIDGSFEIGNLLVITFVSYFGAKLHRPKIIGAGCVIMGV
				GTLLIAMPQFFMEQYKYERYSPSSNSTLSISPCLLESSSQLPV
				SVMEKSKSKISNECEVDTSSSMWIYVFLGNLLRGIGETPIQPL
			Ì	GIAYLDDFASEDNAAFYIGCVQTVAIIGPIFGFLLGSLCAKLY
	l	l	Í	VDIGFVNL/DHF*VSAQLGTRKGVLVCLVFCLLCQSIGRRLSE
		1	ŀ	EHHHSDREKG
232	971	221	1068	OPAGRVEAFCKFHMWAEGMTSLMKAALDLTYPITSMFSGAGFN
232				SSIFSVFKDQQIEDLWIPYFAITTDITASAMRVHTDGSLWRYV
		1		RASMSLSGYMPPLCDPKDGHLLMDGGYINNLPADVARSMGAKV
				VIAIDVGSRDETDLTNYGDALSGWWLLWKRWNPLATKVKVLNM
	ļ		1 .	AEIQTRLAYVCCVRQLEVVKSSDYCEYLRPPIDSYSTLDFGKF
	l	į	1	NEICEVGYQHGRTVFDIWGRSGVLEKMLRDQQGPSKKPASAVL
	[	Ì	j	TCPNASFTDLAEIVSRIEPAKPAM
233	972	133	635	LWVIMFVSYLILTLLHVQTAVLARPGGESIGCDDYLGSDKVVD
233	3/2	123	033	KCGVCGGDNTGCQVVSGVFKHALTSLGYHRVVEIPEGATKINI
	1	ļ		TEMYKSNNYLALRSRSGRSIINGNWAIDRPGKYEGGGTMFTYK
			ĺ	RPNEISSTAGESFLAEGPTNEILDVYVSLDVSGLFFGF
224	973	1	420	ISGGTRSAGPLRRNYNFIAAVVEKVAPSVVHVQLWGRNQQWIE
234	9/3	1	420	VVLQNGARYEAVVKDIDLKLDLAVIKIESNAELPVLMLGRSSD
		1		LRAGEFVVALGSPFSLQNTATAGIVSTKQRGGKELGMKDSDMD
				YVQIDATINYG
	1	<del> </del>	1000	PRVRELKEILDRKGHFSENETRWIIQSLASAIAYLHNNDIVHR
235	974	2	860	DLKLENIMVKSSLIDDNNEINLNIKVTDFGLAVKKQSRSEAML
				QATCGTPIYMAPEVISAHDYSQQCDIWSIGVVMYMLLRGEPPF
				LASSEKLFELIRKGELHFENAVWNSISDCAKSVLKQLMKVDP
	[			LASSEEKLFELIRKGELHFBNAVWNSISDCARSVINQUIRVDF AHRITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVE
l	1			ENTTEEKNKPSTEEKLKSYQPWGNVPETNYTSDEEEEKQVGRI
1	1			
<u></u>	<u> </u>	1		IAAFLPSVKYPHHTWNIFLQICLFVVSL
236	975	1	467	LSISVSDVSLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPQI
1	1	1	1	SGFSSPVMEGDLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYL
		1	1	KEEDANRKTFTVSSTLDFRVDRSDDGVAVICRVDHESLNATPQ
	1	[		VAMQVLEMHYTPSVKIIPSTPFPQEG
237	976	3	417	YNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSPKF
		1		PEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPQ
]		1		MEESELHEVLHHTLTNVDGKAYRTIDGPRSFRQRISPAIA\YT
				YD\SDILKGN



	·		D. diam	A in its annual postide (A = Alexine
SEQ	SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic Acids	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	- Laboration in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
		of amino	of amino	
		acid	acid	
		sequence	sequence	
238	977	2	740	DQDYKYDSTSDDSNFLNPPRGWDHTAPGHRTFETKDQPEYDST
		1	Į.	DGEGDWSLWSVCSVTCGNGNQKRTRSCGYĄCTATESRTCDRPN
			j	CPGIEDTFRTAATEVSLLAGSEEFNATKLFEVDTDSCERWMSC
		ţ		KSEFLKKYMHKVMNDLPSCPCSYPTEVAYSTADIFDRIKRKDF
		i	1	RWKDASGPKEKLEIYKPTARYCIRSMLSLESTTLAAQHCCYGD
	İ			NMQLITRGKGAGTPNLISTEFSAELHYKVDV
239	978	2	612	ESEENGESAMDSTVAKEGTNVPLVAAGPCDDEGIVTSTGAKEE
اردء		1		DEEGEDVVTSTGRGNEIGHASTCTGLGEESEGVLICESAEGDS
				QIGTVVEHVEAEAGAAIMNANENNVDSMSGTEKGSKDTDICSS
	}	]	J	AKGIVESSVTSAVSGKDEVTPVPGGCEGPMTSAASDQSDSQLE
				KVEDTTISTGLVGGSYDVLVSGEVPECEVAH
	070	79	361	VCIICLIFSYYSFDSALQSAKSSLGGNDELSATFLEMKGHFYM
240	979	19	301	YAGSLLLKMGQHGNNVQWRALSELAALCYLIAFQVSLPLGAID
ŀ	1			
		<u> </u>		ISRSLDVF
241	980	2	681	QHPSQEKPQVLTPSPRKQKLNRKYRSHHDQMICKCLSLSISYS
	ļ	1	l	ATIGGLTTIIGTSTSLIFLEHFNNQYPASEVVNFGTWFLFSFP
·			1	ISLIMLVVSWFWMHWLFLGCNFKETCSLSKKKKTKREQLSEKR
1		1	1	IQEEYEKLGDISYPEMVTGFFFILMTVLWFTREPGFVPGWDSF
	i			FEKKGYRTDATVSVFLGFLLFLIPAKKPCFGKKNDGENQEHSL
				GTEPIITWKDF
242	981	1	491	LEREGDKGTPVLRGFSSVSGSWSRRMPPFLLLTCLFITGTSVS
]		1	1	PVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYH
•	Ι.		1	FTGMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQA
	1		<u> </u>	CASFNGNCCLWNTTVEVKACPGGYYVYRLTKPSV
243	982	1	983	CGRTMSDIRHSLLRRDALSAAKEVLYHLDIYFSSQLQSAPLPI
	1			VDKGPVELLEEFVFQVPKERSAQPKRLNSLQELQLLEIMCNYF
				QEQTKDSVRQIIFSSLFSPQGNKADDSRMSLLGKLVSMAVAVC
				RIPVLECAASWLQRTPVVYCVRLAKALVDDYCCLVPGSIQTLK
	1	}		QIFSASPRFCCQFITSVTALYDLSSDDLIPPMDLLEMIVTWIF
İ		1	1	EDPRLILITFLNTPIAANLPIGFLELTPLVGLIRWCVKAPLAY
1		İ	ĺ	KRKKKPPLSNGHVSNKVTKDPGVGMDRDSHLLYSKLHLSVLQV
	1		ļ	LMTLQLHLTEKNLYGPPGADPLRPHG
244	983	32	362	SACSTGPELPGRATRSLTRPANQKGCDGDRLYYDGCAMIAMNG
				SVFAQGSQFSLDDVEVLTATLDLEDVRSYRAEISSRNLAVSAP
				VDTCVGCSSKTWKVAPFVRAWWRP
245	984	158	398	APLSRLCFPQVLVNEGGGFDRASGSFVAPVRGVYSFRFHVVKV
1 2 2 3	75-			YNROTVOVTSALAPIPGSGGWGGGRRGAQLTSGWTLH
246	985	2	707	PHIIGAEDDDFGTEHEQINGQCSCFQSIELLKSRPAHLAVFLR
440	705	4	1,0,	HVVSQFDPATLLCYLYSDLYKHTNSKETRRIFLEFHQFFLDRS
,	1			AHLKVSVPDEMSADLEKRRPELIPEDLHRHYIQTMQERVHPEV
				QRHLEDFRQKRSMGLTLAESELTKLDAERDKDRLTLEKERTCA
	1	1		EQIVAKIEEVLMTAQAVEEDKSSTMQYVILMYMKHLGVKVKEP
1				THE REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
J	]	]	i	RNLEHKRGRIGFLPKIKQSM





SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	
1	1	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
İ		acid	acid	\=possible nucleotide insertion)
		residue	residue of amino	
1		of amino acid	acid	
ł		sequence	sequence	
256	995	2	737	FEQPGNPGDPRVRTPPPWGPHFFALIPSSPKEVPATPSSRRDP
		_		IAPTATLLSKKTPATLAPKEALIPPAMTVPSPKKTPAIPTPKE
1	ŀ	ł		APATPSSKEASSPPAVTPSTYKGAPSPKELLIPPAVTSPSPKE
1		ļ		APTPPAVTPPSPEKGPATPAPKGTPTSPPVTPSSLKDSPTSPA
			ļ	SVTCKMGATVPQASKGLPAKKGPTALKEVLVAPAPESTPIITA
		i .		PTRKGPQTKKSSATSPPICPDPSAKNGSKG
257	996	79	3	FFLKIQGLGWARWLTPVIPVLWEAE
258	997	307	475 ·	AGFGYGLPISRLYAKYFQGDLNLYSLSGYGTDAIIYLKVSLEF
	1	ĺ	ľ	NSKILFLKPLLLL
259	998	26	622	WMRAPMLQKQQAPRMDTPPPEERLEKQNEKLNNQEEETEFKEL
į	1	ļ		DGLREALANLRGLSEEERSEKAMLRSRIEEQSQLICILKRRSD
İ	1	Ì		EALERCQILELLNAELEEKMMQEAEKLKAQGEYSRKLEERFMT
				LAANHELMLRFKDEYKSENIKLREENEKLRLENNSLFSQALKD
1				EEAKVLQLTVRCEALTGELETLKERC
260	999	2	241	DPGASHASVQVQVLKEQLFAGRMPSPFRSCALMGMCGSRSADN
	}			LSCPSPLNVMEPVSFFPLKSLGKGMIQHFRHIVSLV
261	1000	1	620	VTTTTHSVGRGHELQLLNEELRNIELECQNIMQAHRLQKVTDQ
1	1	1		YGDIWTLHDGGFRNYNTSIDMQRGKLDDIMEHPEKSDKDSSSA
	1		İ	YNTAESCRSTPLTVDRSPDSSLPRVINLTNKKNLRSTMAATQS
1	ļ	1		SSGQSSKESTSTKAKTTEQGCSAESKEKVLEGSKLPDQEKAVS
	<u> </u>	<u> </u>		EHIPYLSPYHSSSYRYANIPAHARHYQSYMQLIQ
262	1001	3	420	VWGCLATVSTHKKIQGLPFGNCLPVSDGPFNNSTGIPFFYMTA
				KDPVVADLMKNPMASLMLPESEGEFCRKNIVDPEDPRCVQLTL
· .		i		TGQMIAVSPEEVEFAKQAMFSRHPGMRKWPRQYEWFFMKMRIE
				HIWLQKWYG
263	1002	43	441	QAANMAVARVDAALPPGEGSVVNWSGQGLQKLGPNLPCEADIH
				TLILDKNQIIKLENLEKCKRLIQLSVANNRLVRMMGVAKLTLL
1	1			RVLNLPHNSIGCVEGLKELVHLEWLNLAGNNLIAMEQINSCTA
			<del> </del>	LQHL
264	1003	3	834	FRAAVGAVPEGAWKDTAQLHKSEEAKRVLRYYLFQGQRYIWIE
1				TQQAFYQVSLLDHGRSCDDVHRSRHGLSLQDQMERKAIYGPNV ISIPVKSYPQLLVDEAFSIALWLADHYYWYALCIFLISSISIC
j	]	]		LSLYKTRKQSQTLRDMVKLSMRVCVCRPGGEEEWVDSSELVPG
				DCLVLSQEGGLMPCDAALVAGECMVNDSSLTGESIPVLKTALP
		1		EGLGPYCAETHRRHTLFCGTLILHARAYVGPHVLAVVTRTGMS
	1			REAGLERDPGSAPLKRWS
	1.00	<u> </u>	670	FVGGGLHLHLCLLLCFMLPEDAAMAVLTASNHVSNVTVNYNIT
265	1004	2	670	VERMNRMQGLRVSTVPAVLSPNATLALTAGVLVDSAVEVAFLW
				TFGDGEQALHQFQPPYNESFPVPDPSVAQVLVEHNVTHTYAAP
				GEYVLTVLASNAFENRTQQVLIRSGRVPIVSLECVSCKAQAVY
		j	]	EVSRSSYVYLEGRCLNCSSGSKRGRWAARTFSNKTLVLDETTT
				STGSASM
L		1		STGSWSM



SEQ   Pedicited beginning nucleoided location of mulcoided location of mulcoided location of mulcoide segment properties of the segment containing signal peptide (A = Alanine, and mulcoided location of mulcoide side of mulcoide residue of amino acid residue of amino acid residue of amino acid segment containing, M = Arginine, S = Serine, P-Proline, Q = Glutamine, R = Arginine, S = Serine, Y = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, acid residue of amino acid segment containing with the provided residue of amino acid segment containing with the provided residue of amino acid segment containing with the provided residue of amino acid residue of amino acid segment containing with the provided residue of amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Asparatgine, P = Preline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, acid residue of amino acid segment containing signal peptide (A = Alanine, C = Glutamine, R = Arginine, S = Serine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, acid residue of amino acid segment containing signal peptide (A = Alanine, C = Cysteine, D = Asparagine, R = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, * = Stop Codon, / = possible nucleotide deletion, acid residue of amino acid segment containing signal peptide (A = Alanine, C = Alanine, C = Arginine, S = Serine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, P = Proline, Q = Glutamine, R = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = Tyrotophan, Y = T		4=0	-	D. C.	A to the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of
NO: of Nucleic Arino of Amino Acids of instantian acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of		-			Amino acid segment containing signal peptide (A=Alanine,
Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note   Note					C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of of manical Acids         orresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid res	•				F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Acids Acids Acids Acids of first a mino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence   1005   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1094   2   1093   2   1093   2   1093   2   1093   2   1094   2   1093   2   1093   2   1094   2   1093   2   1094   2   1093   2   1094   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1093   2   1		1			K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence 266 1005 2 1093 PEFLGRLFRGKAATLHVHSDQKPLHDGALGSQQNLVRMKEALR ASTMDVTVVLPSGLEKRSVLNGSHAMMDLLVELGCQNHLMPSH ASTMDVTVVLPSGLEKRSVLNGSHAMMDLLVELGCQNHLMPSH RALEIRSSTYCOPLSFFRYNTLIGTLNWTPFLKERVEPERVYDGPPKVPEKSVRLVVNYLRTOKAVVRVSPEVPLQNTLEVICAKC EVSPEHVVLLRDNIAGEELELSKSLNBLGIKELYAMDNREFT RKSSLGNDETDKEKKKELGFFKVNKRSNSKGCLTTPNSPSMHS RSLTLIGPSLSGISGVSVKSEMKKRRAPPPPGSGPPVQDKAS EKVSLGSQIDLOKKKRRAPAPPPPGPPPPPPPLDIPNRTEDKEEN RKSTMVYCCASFPTQAKRF  267 1006 686 400 VQMENLHSIQPLPAGFK*FLCFSLPSSWDYRCAPPLP/APFFF RKSSLGNDETDKEKKKELGFFKVNKRSNSKGCLTTPNSPSMHS RSLTLIGPSLSGISGVSVKSEMKKRRAPPPPGSGPPVQDKAS EKVSLGSQIDLOKKKRRAPAPPPPGPPPPPPPPPPPPPPPPPPPPPPPPPPP					P=Proline, O=Glutamine, R=Arginine, S=Serine,
amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	Acids	Acids			
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residue of amino acid   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequence   sequenc					
					\=possible nucleotide insertion)
266					
Sequence				1	
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ASTMDVTVILPSGLEKRSVLINGSHAMMDLLVELCLQNHLNPSH HALEIRSSETQPLSFKPNTLIGTLNVHTVFLKEKVPEEKVKP GPPKVPEKSVRLVVNYLRTQKAVVRVSPEVPLQNTLPVICAKC EVSPEHVVLKINNIAGEELELSKSLNELGIKSLYAWDNRRETF RKSSLGNDETDKEKKKFLGFFKVNKRSNSKGCLTTPNSPSPMF SRSLTLGPSISLGSISGVSVKSEMKKRRAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPVQDKAS EKVSLGSQIDLQKKKRRAPAPPPPGSGPPLP/APFFF YTLFLVELGFHHIG*AGLELTSTDLPASAS/ESAGITGMSHRA RMDFFLLKIL  268 1007 1 453 GRFRPPSDEEREPWEFWTQLRLSGHLKFLHYNLMLTAFMENF TFSGEVNVELACRNATRYVULHASRVAVEKVQLAEDRAFGAVP VAGFFLYPQTQVLVVVLNRTLDAQRNYNLKIIYNALIENELLG FFRSSYVLHGERRFLGVTQFSP  269 1008 333 526 KELDFFYNS*RKIKYLRIYLTKEVKDLYKENKTLLKEITDDT M/KKHIPSSWTGRINTVKMTIL QGRGLASLSGIQSGVG  271 1010 16 148 RWNSLTCVVLTFLGHRLLKRFLVPKLRRFLKPQGHPRLLLWFK R  272 1011 1 659 YGEFVTYQGVAVTRSRKEGIAHNYKNETEWRANIDTVAMFTE EDLDLVTLYFGEPDSTGHRYGPESPERREMVRQVDRTVGYHR SIARNHITDRINLIITSDHGMTTVDKRAGDLVEFHKFPNFTFR DIEFELLDYGPNGMLLPKEGRLEKVYDALKDAHPKLHVVKKEA FPEAFHYANNPRVTPLLMYSDLGYVIHGVSRLLEAPPPGAPSP GSGS  273 1012 146 413 RIPLLRLSSTYRSKGFDVTVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIAITIFESKNFFLPGIKMNGILGLSYATLAKPSSSLE TFF DIEFELLDYGPNGMSLPKEGRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCSFCPDLH*CIRBDVXPENIITHTSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGMLWEYAPGGTLAEFIQKECNSLLEEETILHFFVQILLALH HVPHHLLHRDLKYONILLDKRMWVKEGGFGISKLLSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	566	1005	•		DEDT ON THOUSANT HIM CHOKRI HOGALGSOOM VEMERALE
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SIARNHLTDRLNLIITSDHGMTTVDKRAGDLVEFHKFPNFTFR DIEFELLDYGPNGMLLPKEGRLEKVYDALKDAHPKLHVYKKEA FPEAFHYANNPRVTPLLMYSDLGYVIHGVSRLLEAPPPGAPSP GSGS  273 1012 146 413 RIPLLRLRSSTYRSKGFDVTVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK 276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	272	1011	1	659	
DIEFELLDYGPNGMLLPKEGRLEKVYDALKDAHPKLHVYKKEA FPEAFHYANNPRVTPLLMYSDLGYVIHGVSRLLEAPPPGAPSP GSGS  273 1012 146 413 RIPLLRLRSSTYRSKGFDVTVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK 276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	j	1	]	]	
FPEAFHYANNPRVTPLLMYSDLGYVIHGVSRLLEAPPPGAPSP GSGS  273 1012 146 413 RIPLLRLRSSTYRSKGFDVTVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK 276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	ļ	1		1	
GSGS  273 1012 146 413 RIPLRLRSSTYRSKGFDVTVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF		1		1	
273 1012 146 413 RIPLERESTYRSKGFDVTVKHSHGSWTGFGGEDLATIPKGL NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	1				
NTYFLVNIATIFESKNFFLPGIKWNGILGLSYATLAKPSSSLE TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF				<u></u>	
TFF  274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	273	1012	146	413	
274 1013 3 251 IKSYSGPNGRSCQIWQRLRWGSRELLLGWKLSHSFSTCPFQFP DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF			ļ		§ .
DIVEFCEAMANAGKTVIVAALDGTFQRKVRRLIQVWSWD  275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	1				
275 1014 326 651 YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	274	1013	3	251	
SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	1		1	1	
SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE \LLSGKCLWWPGKS/DMLDQLYLIRK  276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	275	1014	326	651	YCFCFDLLH*CIHRDVKPENILITKHSVIKLCDFGFARLLTGP
276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL 277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF					SDYYTDYVATRWYRSPELPVGDTQY\GPPV\DVW\AIGCVSAE
276 1015 224 435 RGWALDWIGADLSLHLQEEVETEVAWEECGHVLLSLCYSSQQG GLLVGVLRCAHLAPMDANGYSDPFVRL 277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	1				\LLSGKCLWWPGKS/DMLDQLYLIRK
GLLVGVLRCAHLAPMDANGYSDPFVRL  277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	276	1015	224	435	
277 1016 2 429 GGILAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALH HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF					
HVHTHLILHRDLKTQNILLDKHRMVVKIGDFGISKILSSKSKA YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	277	1016	12	429	
YTVVGTPCYISPELCEGKPYNQKSDIWALGCVLYELASLKRAF	[ ~ ′ ′	1,1010	*	1 223	
1 i i i	1	1	1	1	VWMICTPCVTCDELCECKDVMCKCDTWALCCVILVELACI.KDAF
					l e e e e e e e e e e e e e e e e e e e
<u></u>	L	<u></u>	1		DAWNIEWIIATIKTA



000	CEO I	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Giutannic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
	<b>l</b> 1	residue	residue	,
		of amino	of amino	
	1	acid	acid	,
ļ		sequence	sequence	
278	1017	1	262	VQCGGIHQVSGAVVVSGLLQGMMGLLGSPGHVFPHCGPLVLAP
		ŀ		SLVVAGLSAHREVAQFCFTHWGLALLYVSPERRGMVPSGGVWG
	ł	Ì		α
279	1018	1	480	PRMTGSTHASAPSYGGSCRNNLFYREETYTPKAETDEMNEVET
			ł	APIPEENHVWLQPRVMRPTKPKKTSAVNYMTQVVRCDTKMKDR
	l		1	CIGSTCNRYQCPAGCLNHKAKIFGSLFYESFASICRAAIHYGI
	ł	1		LDDKGGLVDITRNGKVPFFVKSERHGVQSLR
280	1019	271	792	VPQNIICAFFCVPCRFASTIPFWGLTLHLQHLGNNVFLLQTLF
200	1015		1	GAVTLLANCVAPWALNHMSRRLSQMLLMFLLATCLLAIIFVPQ
	}		ļ	EMOTLRVVLATLGVGAASLGITCSTAQENELIPSIIRGRATGI
	ļ		ļ	TGNFANIGGALASLVMILSIYSRPLPWIIYGVFAILSGLVVLL
	Ì	ļ	1	LP
	1000	2	679	VLVSRDHMKSAQQFFQLVGGSASECDTIPGRQCMASCFFLLKQ
281	1020	4	019	FDDVLIYLNSFKSHFYNDDIFNFNYAQAKAATGNTSEGEEAFL
	1	ļ	1	LIOSEKMKNDYIYLSWLARGYIMNKKPRLAWELYLKMETSGES
1		1	<b>1</b>	FSLLQLIANDCYKMGQFYYSAKAFDVLERLDPNPEYWEGKRGA
j	]	}	]	CVGIFQMIIAGREPKETLREVLHLLRSTGNTQVEYMIRIMKKW
1 .	1	1		AKENRVSILK
		<u> </u>	ļ	LKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
282	1021	3	359	LFPDKKDRQNSEREAGKKHKVREITVHQRVTVDFVALHIVTLL
	İ		i	
				LPQLSHFFCLRIERVIIYLEKPIFARLRWLMP
283	1022	3	538	GVPRNLPSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNC
			1	RRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSW
		1	1	LNASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNL
(		Ì		SFNYQKRVSFAHLVSGPPFLRGSLGRPLKGAGTWHGNLSFPLH
į		ļ		FEWGKT
284	1023	3	442	ILFAALIWSSFDENIEASAGGGGGSSIDAVMVDSGAVVEQYKR
		1	1	MQSQESSAKRSDEQRKMKEQQAAEELREKQAAEQERLKQLEKE
1	1		ł	RLAAQEQKKQAEEAAKQAELKQKQAEEAAAKAAADAKAKAEAD
	1		1	AKAAEEAAKKAAADAKK
285	1024	1	119	AMEIVHEPRDLERYMREAVKVSNDSPVLLDRFLNDAIEC
286	1025	67	227	MLSPGYDYGYVCVEFSLLEDAIGCMEANQVALYFGQMMLEGYI
	1	1	1	FLYMGREGFK
287	1026	2	1101	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRL
	1			KCVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRP
	1	1		EDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNT
ļ	1		1	TVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVG
1	1			GQKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGAN
1				TMGYSFRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPA
1				GAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSG
1		1		DKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLY
1				PKLYT\DIPHHTHTPHPPAN
1000	1225	3	96	NFHFTGKCLFMSGLSEVQLTHMDDHTLPGY
288	1027		1 20	WENT TAKENT IN ORDER FROM



CEC 1	SEC.	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ ID	SEQ ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine; I=Isoleucine,
of	of	location	location	P=Pnenylalanine, G=Glycine, H=Histidile, 1=1soleuchie,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
		to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	
į		of amino	of amino	
		acid	acid	·
289	1028	sequence 95	sequence	SPRKRKTRHSTNPPLECHVGWVMDSRDHGPGTSSVSTSNASPS
289	1028	35	1307	EGAPLAGSYGCTPHSFPKFQHPSHELLKENGFTQQVYHKYRRR
<u>'</u>		}		CLSERKRLGIGOSQEMNT
290	1029	1	359	PGSGGSAGGRDGSAYQGALLPREQFAAPLGRPVGTSYSATYPA
290	1029	1 *	333	YVSPDVAQSWTAGPFDGSVLHGLPGRRPTFVSDFLEEFPGEGR
<u>'</u>		}		ECVNCGALSTPLWRRDGTGHYLCNACGLYHKMN
291	1030	2	513	PDHRHGALWWWYSCGVLPVTVSRNEGDERNQVLTLYLWIRQEW
291	1030	~	323	TDAYLRWDPNAYGGLDAIRIPSSLVWRPDIVLYNKYCLS/AAP
}	]	Ì	}	PLSYPSLDLPLAVGV**SPLPTT*PGCHAALEAFPQDPSKLPS
}	Ì	1		TOPLHGTPTLGYPRPAQAERLLGTYCVVQGRCLNHKGLSRAHF
292	1031	<del> </del>	595	YALTGALVIVTGMVMGNIADYFNLPVSSMSNTFTFLNAGILIS
292	1031	-	1 232	IFLNAWLMEIVPLKTQLRFGFLLMVLAVAGLMFSHSLALFSAA
ł	l	1		MFILGVVSGITMSIGTFLVTQMYEGRQRGSRLLFTDSFFSMAG
Ì	1	İ		MIFPMIAAFLLARSIEWYWVYACIGLVYVAIFILTFGCEFPAL
l	1	1	}	CSHATKLGTASSYPSLDVVQLRTLNA
293	1032	71	479	MAKVGLKTEHYDRYPHMFSGGQRQRIAIARGLMLDPDVVIADE
293	1032	\	1 3/3	PVSALDVSVRAQVLNLMMDLQQELGLSYVFISHDLSVVEHIAD
1		}	j	EVMVMYLGRCVEKGTKDQIFNNPRHPYTQALLSATPRLNPDDR
İ	Ì			RERIKLSX*
294	1033	2	427	SATLERVLNHPDETQARRLMTLEDIVSGYSNVLISLADSQGKT
	1	-	'	VYHSPGAPDIREFTRDAIPDKDAQGGEVYLLSGPTMMMPGHGH
1	ļ	ļ		GHMEHSNWRMINLPVGPLVDGKPIYTLYIALSIDFHLHYINDL
{	1			MNKLIMTASVII
295	1034	3	342	VLAYPGIKVSTAEARAILPAQYRRQDCIAHGRHLAGFIHACYS
1 233		}		ROPELAAKLMKDVIAEPYRERLLPGFRQARQAVAEIGAVASGI
}		}	}	SGSGPTLFALCDKPETAQRVADWLGK
296	1035	2	279	GOOORVALARALILKPKVLLFDEPLSNLDANLRRSMRDKIREL
250	1000	~		QKQFDITSLYVTHDQSEAFAVSDTVLVMNKGHIMQIGSPQDLR
{	į	{	1	VRRLNW
297	1036	3	157	AVHYLERVRIAEHAHKFPGQISGGQQQRVAIARSLCMKPKIML
}	1	"	]	FDEPTSAL
298	1037	+ <del>1</del>	217	APYDAENYFDYDNLNNGPSLQHWFGVDSLGRDIFSRVLVGAQI
-	1	-	1	SLAAGVFAVFIGAAIGTLLGLLAGYYEGW
299	1038	3	570	VFCLIADLDPIDELVDFPIVYASALNGIAGLDHEDMAEDMTPL
1233	1 2333	1		YQAIVDHVPAPDVDLDGPFQMQISQLDYNSYVGVIGIGRIKRG
				KVKPNQQVTIIDSEGKTRNAKVGKVLGHLGLERIETDLARAGD
1				IVAITGLGELNISDTVCDTQNVEALPALSVDEPTVSMFFCVNT
1				SPFCGKEGKFVTSRQI
300	1039	+1	366	QGTRAESQGSSKDKTRLAFAGLKFGDYGSIDYGRNYGVAYDIG
330	1 233	1		AWTDVLPEFGGDTWTQTDVFMTQRATGVATYRNNDFFGLVDGL
				NFAAQYQGKNDRSDFDNYTEGNGHGFGFSATYEYEG
301	1040	1 3	201	DTYSVSIPLGATINMAGAAITITVLTLAAVNTLGIPVDLPTAL
301	1040	]	201	LLSVVASLCACGASGVAGGSLL
L	ــــــــــــــــــــــــــــــــــــــ	ــــــــــــــــــــــــــــــــــــــ	<u> </u>	

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SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
·		residue	residue	(-possiole nucleodide matrices)
		of amino	of amino	
		acid	acid	
}	}	sequence	sequence	
302	1041	1	140	ANAQQGLPSGITLKLNNLVDKGLVDRLYAASSSGVPVNLLVRG
]			1	TCS .
303	1042	2	442	ARMTLIPGTHLLENIHNIWVNGVGTNSAPFWRMLLNSFVMAFS
303		] _	\	ITLGKITVSMLSAFAIVWFRFPLRNLFFWMIFITLMLPVEVRI
ł	}		1	FPTVEVIANLOMLDSYAGLTLPLMASATATFLFRKLNMSGPDK
Ì	1	•	<b>!</b>	VVPAARISGYGPRVRKQ
304	1043	2	403	CAKCLRDADECPSGAFERIGRDISLDALEREVMKDDIFFRTSG
304	1043	-	1 403	GGVTLSGGEVLMQAEFATRFLQRLRLWGVSCAIETAGDAPASK
		ļ	•	LLPLAKLCDEVLFDLKIMDATQARDVVKMNLPRVLENLRLLVS
}				EGVN
<u></u>	1 2 2 4 4	<del> </del>	346	YLLLFVCFLVMSLLVGLVYKFTAERAGKQSLDDLMNSSLYLMR
305	1044	1	340	SELREIPPHDWGKTLKEMDLNLSFDLRVEPLSKYHLDDISMHR
1			1	LRGGEIVALDDQYTFLQRIPRSHYVLAVG
	<u> </u>	<u> </u>	<del> </del>	VELFLSDEGDDVVIEVADQGCGVPESLRDKIFEQGVSTRADEP
306	1045	1	207	
		<u> </u>		GEHGIGLYLIASYVTRCGGVITLEDN
307	1046	3	213	DAIIAPDANALPAAAQAAENLKNDKVAIVGFSTPNVMRPYVER
<u></u>	1	<u></u>	<u> </u>	GTVKEFGLWDVVQQGKISVYVADALQ
308	1047	1	129	YIVVTGKTHCGTPLTTVTGDATQSGYLTLNLPEMWEVSGYNRV
309	1048	271	46	XEGVEPDINASKTRQQLNDVAGKMKIIEARLSALTNNQTKSLK
	J			LNPVALPKVASQLLDELGYSLLARRADLQSAHX*
310	1049	16	253	ENIAEEYATKRYRSNVINWGMLPLQMAEVPTFEVGDYIYIPGI
		l	l	KAALDNPGTTFKGYVIHEDAPVTEITLYMESQEART
311	1050	2	299	LQTEIGSMVYAVKPGDGSAREQAASCQRVIGGLANIAEEYATK
1	1	1		RYRSNVINWGMLPLQMAEVPTFEVGDYIYILGFKAAKYSPGTA
1	1			FTVYAISGYGPRI
312	1051	1	344	TLEDLLMALDGEQHLQQQVSEKVLADNVLIAPGSVKPDATFWS
1		}	į	ALIQDRYNVMTCIEKDACVLVEQDLNSDGQAERILFAFNDDRV
1	,	1	j	IVYGFDSDRKEWDALDMSLLPNEITKEK
313	1052	2	630	ESNSRCRKMPGERCRGGPARLSLLLDLPTRPLPHPRQVIDFGS
1		1	į.	ASIFSEVRYVKEPYIQSRFYRAPEILLGLPFCEKVDVWSLGCV
	1	1	1	MDELHLGWPLYPGNNEYDQVRYICETQGLPKPHLLHAACKAHH
	1	· ·	1	FFKRNPHPDAANPWQLKSSADYLAETKVRPLERRKYMLKSLDQ
1	j		1	IETVNGGSVASRLTFPDREALAEHADLKSMVEL/MKRLL
314	1053	+1	302	RLVKKRVECRQCGKAGRNQSTLKTHMRSHTGEKPYECDHCGKA
743	1 -000		1	FSIGSMLNVHRRIHTGEKPYECLVCGEAFSDHSSLRSHVKTHR
1			1	GEKLFVSSVWKRLQ
315	1054	1318	730	CGPGFSLSFFFLRWSF\ALVAQAGVQWHDLGSLQPPAPGFKRF
1313	1034	1310	1	SSLSLLSRWDYRHAHARLIFVFLVEMGFLHVGQAGLELPTSGD
ł	1	1	1	PPTSASQSARITGVTTPLGTFFFFLRWSFALVAQAGGQCLDLG
1	1	1		SLQLPPPGFKRLVCHFQTPQKHRCSCQAPGDCLQESFVMTGCV
1	1	}	1	LRTVSESVQRANAGAGAETVQGL
<b>I</b>	_1	1		TIKI VORO VQIMIMONONE I VQUI

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \perpossible nucleotide insertion)
316	1055	2486	1429	MGNAAAAKKGSEQESVKEFLAKAKEDFLKKWESPAQNTAHLDQ FERIKTLGTGSFGRVMLVKHKETGNHYAMKILD*QKVGKLKQI EHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVPGGEM FSHLRRIGRFSEPHARFYAAQĪVLTFEYLHSLDLIYRDLKPEN LLIDQQGYIQVTDFGFAKRVKGRTWTLCGTPEYLAPEIILSKG YNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRF PSHFSSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATT DWIAIYQRKVEAPFIPKFKGPGDTS\NFDDYEEEEIRV\SINE KFG\KEFSEF
317	1056	867	461	SSSRSSHGDSPPHSQTPCDTNRGLDTKH*/DSQSIEEKDSSQS E*NRIERRKEVERILQTNSDYM*HWSN*PENILPKKFFSKHQK CTATLSMRNTSIM/KKEGLF*AQFPSLLLSHLPAVGLGIYTGT HLTTSTSTF
318	1057	544	784	TFHSSLEKNILQPCR*RRA\ICLPLLL*PSVPLLAPQYFSDLR NSIVNSQPPEKQQAMHLCFENLMEGIERNLLTKNRDR
319	1058	1606	228	GTSGVQQEISRLTNENLDLKELVEKLEKNERKLKKQLKIYMKK AQDLEAAQALAQSERKRHELNRQVTVQRKEKDFQGMLEYHKED EALLIRNLVTDLKPQMLSGTVPCLPAYILYMCIRHA\DYTNDD LKVHSLLTSTINGIKKVLKKHNDDFEMTSFWLSNTC\RLLHCL KQYSGDEGFMTQNTAKQN\EHCLKNFDLTEYRQV\L\SDLSIQ IYQQLIKIAEGVLQPMIVSAMLEN*SIQGLSGVKPTGSQKHSS SMADEDNSYRLEAIIRQMNAFHTVMCDQGLDPEIILQVFKQLF YMINAVTLNDLLLRKDVCSWSTGMQLRYNISQLEEWLRGRNLH QSGAVQTMEPLIQAAQLLQLKKKTQEDAEAICSLCTSLSTQQI VKILNLYTPLNEFEERVTVAFIRTIQAQLQERNDPQQLLLDAK HMFPVLFPFNPSSLTMDSIHIPACLNLEFLNEV HEENTILKAAEVQVPPK*VVTPEAKAFI*RCLAYQKEDCIDAQ
	1		}	QLACDP\YLLHYIQKLVFVSSPAGAAIASTFGVSNSCSSN
321	1060	1332	500	GTTDEIMTRWARVSTTYNKRPLPATSWEDMKKGSFEGTSQNLP KRKQLEANRLSLKNDAPQAKHKKNKKKKEYLNEDVNGFMEYLR QNSQMVHNGQIIATDSEEVREEIAVALKKDSRREGRRLKRQAA KKNAMVCFHCRKPGHGIADCPAALENQDMGTGICYRCGSTEHE ITKCKAKVDPALGEFPFAKCFVCGEMGHLSRSCPDNPKGLYAD GGGCKLCGSVEHLKKDCPESQNSERMVTVGRWAKGMSADYEEI LDVPKPQKPKTKIPKVVNF
322	1061	384	102	DHVRKSLLKNRAENIVNIFKCNVVSLPNLPAFGQAQWLTPVIP ALWEAEVGGS*GQEIETILANAVK/SPFLLKIQKKKISRAWWR AP/VSPRYSGG

		Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
323	1062		777	SDAWADAWARSLSVSPSSYPELHTEVPLSVLILGLLVVFILSV CFGAGLFVFVLKRRKGVPSVPRNTNNLDVSSFQLQYGSYNTET HDKTDGHVYNYIPPPVVQMCQNPIYMAGREGRPSSLLPKPGKE FQLLGNLEEKKEEPATPAYTISATELLEKQATPREPELLYQNI AE/PSQGTS/TAQA*STITFVPYLKGQFAPSYESRRQNQDRIN KTVLYGTPRKCFVGQSKPNHPLLQAKPQSEPDYLEVLEKQTAI SQL
324	1063	1	1496	ALCHIAVGQQMNLHWLHKIGLVVILASTVVAMSAVAQLWEDEW EVLLISLQGTAPFLHVGAVAAVTMLSWIVAGQFARAERTSSQV TILCTFFTVVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGA PMLAPEHTLMSFRKALEQKLYGLQADITISLDGVPFLMHDTTL RRTTNVEEEFPELARRPASMLNWTTLQRLNAGQWFLKTDPFWT ASSLSPSDHREAQNQSICSLAELLELAKGNATLLLNLRDPPRE HPYRSSFINVTLEAVLHSGFPQHQVMWLPSRQRPLVRKVAPGF QQTSGSKEAVASLRRGHIQRLNLRYTQVSRQELRDYASWNLSV NLYTVNAPWLFSLLWCAGVPSVTSDNSHTLSQVPSPLWIMPPD EYCLMWVTADLVSFTLIVGIFVLQKWRLGGIRSYNPEQIMLSA AVRRTSRDVSIMKEKLIFSEISDGVEVSDVLSVCSDNSYDTYA NSTATPVGPRGGGSHTKTLIERSGR
325	1064	1899	776	NSADYGDGPDSSDADPDSGTEEGVLDFSDPFSTEVKPRILLMG LRRSGKSSIQKVVFHKMSPNETLFLESTNKICREDVSNSSFVN FQIWDFPGQIDFFDPTFDYEMIFRGTGALIFVIDSQDDYMEAL ARLHLTVTRAYKVNTDINFEVFIHKVDGLSDDHKIETQRDIHQ RANDDLADAGLEKIHLSFYLTSIYDHSIFEAFSKVVQKLIPQL PTLENLLNIFISNSGIEKAFLFDVVSKIYIATDSTPVDMQTYE LCCDMIDVVIDISCIYGLKEDGAGTPYDKESTAIIKLNNTTVL YLKEVTKFLALVCFVREESFERKGLIDYNFHCFRKAIHEVFEV RMKVVKSRKVQNRLQKKKRATPNGTPRVLL
326	1065	1181	346	RTRGRDPGAGFRRTANKRCCRRRFLIGCGWLPLRSDWPLVSKM LSKGLKRKREEEEEKEPLAVDSWWLDPGHAAVAQAPPAVASSS LFDLSVLKLHHSLQQSEPDLRHLVLVVNTLRRIQASMAPAAAL PPVPSPPAAPSVADNLLASSDAALSASMASLLEDLSHIEGLSQ APQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGL FEDIDTSMYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELD YLMDVLVGTQALERPPGPGR

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SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Açids	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	<b>i</b> !	to first	to first	I = Infeonine, V = Vallie, W = Tryptophan, I = Tytoshie,
	<u> </u>	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	1	acid	acid	\=possible nucleotide insertion)
	1	residue	residue	
	1	of amino	of amino	
		acid	acid	
	1	sequence	sequence	
327	1066	1844	337	LQEVKARRNTLHKEKDHLVNDYEQNMKLLQTKYDADINLLKQE
	}	}		HALSASKASSMIEELEQNVCQLKQQLQESELQRKQQLRDQENK
•	ł	<u> </u>	i	FOMEKSHLKHIYEKKAHDLQSELDKGKEDTQKKIHKFEEALKW
	ł	ł	ł	KKWROI*LDPN/LLREKQSKEFLWQLEDIRQRYEQQIVELKLE
	į	1	ļ	HEQEKTHLLQQHNAEKDSLVRDHEREIENLEKQLRAANMEHEN
		Ì	t	QIQEFKKRDAQVIADMEAQVHKLREELINVNSQRKQQLVELGL
	1	1	}	LREEEKQRATREHEIVVNKLKAESEKMKIELKKTHAAETEMTL
	1	}	1	PRESERVICATION TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
	1	1	1	EKANSKLKQIEKEYTQKLAKSSQIIAELQTTISSLKEENSQQQ
	1		ł	LAAERRLQDVRQKFEDEKKQLIRDNDQAIKVLQDELENRSNQV
			}	RCAEKKLQHKELESQEQITYIRQEYETKLKGLMPASLRQELED
ļ	1	1	ļ	TISSLKSQVNFLQKRASILQEE/RDYISRQKVQPISR*LHERM
1	1	1	}	QRMRISRLCCGTSSSRFEDLDIVNCEISGIF
328	1067	1149	238	VINLVYLISSPRPELKPVDKESEVVMKFPDGFEKFSPPILQLD
320	1007			EVDFYYDPKHVIFSRLSVSADLESRICVVGENGAGKSTMLKLL
[	{	ĺ	1	LGDLAPVRGIRHAHRNLKIGYFSQHHV\EQL\DLNVQCLWELA
	1	1	1	GHASFPG\RPEEEY\RHQLGFGMGISGEL\AMRPLCQPVLGAR
1	1	1	1	KKPKWPFAQMDYCPAPTFYIL\DEPTN\HLGHGRAIEALGPCL
	1	ì	l	QTISGVGVILVSHE*SALSRLVCRE\LWVC*G\GGVTRVERKD
	1	1	1	QTISGVGVILVSHE SALSKLVCKE (LWVC G GGVIRVEKIG)
ĺ		1	1	FDQYRALLQGTVSAREGFPLGPPRLKDSPRDMGLVSQTPWGHH
l l				VGYPLPGRG
329	1068	26	674	CSAVEVKMAARTAFGAVCRRLWQGLGNFSVNTSKGNTAKNGGL
}	1			LLSTNMKWVQFSNLHVDVPKDLTKPVVTISDEPDILYKRLSVL
1	1			VKGHDKAVLDSYEYFAVLAAKELGISIKVHEPPRKIERFTLLQ
ł	₹.		1 ,	SVHIYKKHRVQYEMRTLYRCLELEHLTGSTADVYLEYIQRNLP
1	1	ì	,	EGVAMEVTKFCFFIFL\TQLEQLPEHIKEPIWETLSEEKEESK
1		ł		S
1-33	1000	2105	1283	DFWDTAGQERFQSMHASYYHKTHACIMVFDVQRKVTHRNLSTW
330	1069	2105	1203	YTELREFRPEIPCIVVANKIDGGAIPAPGC*QFTGDLPSYISS
1		ł	-	SIPRAGNLQ*LVLPPTIRYNPWLVACILPTL*RSQLSRPALFP
1				
İ	1	1	1	RHRSLLTELFLGPVSQSSLPIPLSGMKASSGPPLQTFFPSLDR
1		1	1	QTNVLPSLY\ADINVTQKSFNFAKKFSLPLYFVSAADGTNVVK
İ		1	ì	LFNDAIRLAVSYKQNSQDFMDEIFQELENFSLEQEEEDVPDQE
		1	1	QSSSIETPSEEVASPHS
331	1070	1	1109	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWIL
1		-	1	GRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGW
}		1	}	GCMLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAF
ł		l	1	IDRKDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVF
j		l .	1	DTWSSLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDR
1	1	1	1	HCNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTDINEAYVETLK
	}			HCNGFPAGAEVINKPSPWKPDVIDIPHKIGHIDIMEAIVETHK
}	1		}	HCFM\MPQSLGVIGGKPNSAH\YFIG*VG\EELIYLDPHTTQP
	1			AVEPTDGCFIPDESFHCQHPPCRMSIAELDPSIAVVRGGHLST
1	}	ì		QAFGAECCLGMTRKTFGFLRFFFSMLG
332	1071	39	284	ALCVVPFNTFHN\DFLLLDKEGTLDPVMDSFSTHWTTIGPADM
1		}		FFS\FRQHYKNFKSHGTNPSKSVWAHATCQSCAFPNLLGW
				<u> </u>

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
333	1072	2	1484	TRLAEFGTRDPCAQAPCEQQCEPGGPQGYSCHCRLGFRPAEDD PHRCVDTDECQIAGVCQQMCVNYVGGFECYCSEGHELEADGIS CSPAGAMGAQASQDLGDELLDDGEDEEDEDEAWKAFNGGWTEM PGILWMEPTQPPDFALAYRPSFPEDREPQIPYPEPTWPPPLSA PRVPYHSSVLSVTRPVVVSATHPTLPSAHQPPVIPATHPALSR DHQIPVIAANYPDLPSAYQPGILSVSHSAQPPAHQPPMISTKY PELFPAHQSPMFPDTRVAGTQTTTHLPGIPPNHAPLVTTLGAQ LPPQAPDALVLRTQATQLPIIPTAQPSLTTTSRSPVSPAHQIS VPAATQPAALPTLLPSQSPTNQTSPISPTHPHSKAPQIPREDG PSPKLALWLPSPAPTAAPTALGEAGLAEHSQRDDRWLLVALLV PTCVFLVVLLALGIVYCTRCGPHAPNKRITDCYRWVIHAGSKS PTEPMPPRGSLTGVQTCRTSV
334	1073		1406	LRVRRPHLPAPPALRARRSDRRSSRAPAAFPPRPHASPAPG PAMAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPA TTGAVVTISASLVAKDNGSLALPADAHLYRFHWIHTPLVLTGK MEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGFVVL PITEFLVGDLVVTQNTSLPWPSSYLTKTVLKVSFLLHDPSNFL KTALFLYSWDFGDGTQMVTEDSVVYYNYSIIGTFTVKLKVVAE WEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVLGPTLIQTF QKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAY NLTHTFRDPGDYCFSIRAENIISKTHQYHKIQVWPSRIQPAVF AFPCATLITVMLAFIMYMTLRNATQQKDMVENPEPPSGVRCCC QMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV
335	1074	1	866	VVEFAFQLSSVSVCLTVSFGWQLGTVSSCLSRDWFLKGNLLII IVSVLIILPLALMKHLGYLGYTSGLSLTCMLFFLVSVIYKKFQ LGCAIGHNETAMESEALVGLPSQGLNSSCEAQMFTVDSQMSYT VPIMAFAFVCHPEVLPIYTELCRPSKRRMQAVANVSIGAMFCM YGLTATFGYLTFYSSVKAEMLHMYSQKDPLILCVRLAVLLA\V TLTVPVVLFPIRRALQQLLFPGKAFSWPRHVAIALILLVLVNV LVICVPTIRDIFGVIGSTSAPSLIFILPSCI
336	1075	3	825	GAGSKSSMMQLMHLESFYEK\PPPGLIKEDDTKPEDCIPDVPG NEHAREFLAHTPTKGLWMPLEKEVKVKH/CTFHWIAS*FLGDG KFIPKATRLKDVWVSN*FTCLFWDLTRFIHDCIFF*NWSLMNK NFNIIY*FFISLR*NTLILQKYFPFSLLLGWHCKWYGHRTGYK ECPFFIKDNQKLQQFRVAHEDFMYDIIRDNKQHEKNVRIQQLK QLLEDSTSGEDRSSSSSSEGKEKHKKKKKKEKHKKRKKEKKKK KKRKHKSSKSNEGSDSE

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  EIAGAAENMLGSLLCLPGSGSVLLDPCTGSTISETTSEAWSV
337	1076	3		EVLPSDSEAPDLKQEERLQELESCSGLGSTSDDTDVREVSSRP STPGLSVVSGISATSEDIPNKIEDLRSECSSDFGGKDSVTSPD MDEITHDFLYILQPKQHFQHIEAEADMRIQLSSSAHQLTSPPS QSESLLAMFDPLSSHEGASAVVRPKVHYARPSHPPPDPPILEG AVGGNEARLPNFGSPMF*LPAEMEAFKQRHS/YTPERLVRSRS S\DIVSSVRRPMSDPSWNRRP\GNEERELPPAAAIGATSLVAA PHSSSSSPSKDSSRGETEERKDSDDEKSDRNRPWWRKRFVSAM PKAPIPFRKKEKQEKDKDDLGPDRFSTLTDDPSPRLSAQAQVA EDILDKYRNAIKRTSPSDGAMANYESTEVMGDGESAHDSPRDE ALQNISADDLPDSASQAAHPQDSAFSYRDAKKKLRLALCSADS VAFPVLT\HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQDK NLMAQLQETMRCVCRFDNRTCRKLLASIAEDYRKRAPYIAYLT RCRQGLQTTQAHLERLLQRVLRDKEVANRYFTTVCVRLLLESK EKKIREFIQDFQKLTAADDKTAQVEDFLQFLYGAMAQDVIWQN ASEEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILRDQVLHEH IQRLSKVVTANHRALQIPEVYLREAPWPSAQSEIRTISAYKTP RDKVQCILRMCSTIMNLLSLANEDSVPGADDFVPVLVFVLIKA NPPCLLSTVQYISSFYASCLSGEESYWWMQFTAAVEFIKTIDD RK
338	1077	536	1305	WPMSLARGHGDTAASTAAPLSEEGEVTSGLQALAVEDTGGPSA SAGKAEDEGEGGREETEREGSGGEEAQGEVPSAGGEEPAEEDS EDWCVPCSDEEVELPADGQPWMPPPSEIQRLYELLAAHGTLEL QAEILPRRPPTPEAQSEEERSDEEPEAKEEEEEKPHMPTEFDF DDEPVTPKDSLIDRRRTPGSSARSQKREARLDKVLSDMKRHKK LEEQILRTGRDLFSLDSEDPSPASPPLRSSGSSLFPRQRKY
339	1078	2	1771	LGRGTFGQVV*CWKRGTNEIVAIKILKNHPSYARQGQIEVSIL ARLSTESADDYNFVRAYECFQHKNHTCLVFEMLEQNLYDFLKQ NKFSPLPLKYIRPVLQQVATALMKLKSLGLIHADLKPENIMLV DPSRQPYRVKVIDFGSASHVSKAVCSTYLQSRYYRAPEIILGL PFCEAIDMWSLGCVIAELFLGWPLYPGASEYDQI/RYISQTQG LPAEYLLSAGTKTTRFFNRDTDSPYPLWRLKTPDDHEAETGIK SKEARKYIFNCLDDMAQVNMTTDLEGSDMLVEKAVRREFIDLL KKMLSIDSVKRFSPVGSLNHPFVTMSLFLDFPHSTHVKSCFQN MEICKRRVNMYDTVNQSKTPFITHVAPSTSTNLTMTFNNQLTT VHNQPSAASMAAVAQRSMPLQTGTAQICARPDPFQQALIVCPP GFQGLQASPSKHAGYSVRMENAVPIVTQAPGAQPLQIQPGLLA QQAWPSGTQQILLPPAWQQLTGVATHTSVQHAAVIPETMAGTQ QLADWRNTHAHGSHYNPIMQQPALLTGHVTLPAAQPLNVGVAH VMRQQPTSTTSSRKSKQHLYCGRARVSKIASR



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
340	1079	2	2721	EFAICRYPLGMSGGQIPDEDITASSQWSESTAAKYGRLDSEEG DGAWCPEIPVEPDDLKEFLQIDLHTLHFITLVGTQGRHAGGHG IEFAPMYKINYSRDGTRWISWRNRHGKQVLDGNSNPYDIFLKD LEPPIVARFVRFIPVTDHSMNVCMRVELYGCVWLDGLVSYNAP AGQQFVLPGGSIIYLNDSVYDGAVGYSMTEGLGQLTDGVSGLD DFTQTHEYHVWPGYDYVGWRNESATNGYIEIMFEFDRIRNFTT MKVHCNNMFAKGVKIFKEVQCYFRSEASEWEPNAISFPLVLDD VNPSARFVTVPLHHRMASAIKCQYHFADTWMMFSEITFQSDAA MYNNSEALPTSPMAPTTYDPMLKVDDSNTRILIGCLVAIIFIL LAIIVIILWRQFWQKMLEKASRRMLDDEMTVSLSLPSDSSMFN NNRSSSPSQGSNSTYDRIFPLRPDYQEPSRLIRKLPEFAPGE EESGCSGVVKPVQPSGPEGVPHYAEADIVNLQGVTGGNTYSVP AVTMDLLSGKRCGCGREFPPGKLLTFKEKLGEGQFGEVHLCEV EGMEKFKDKDFALDVSANQPVLVAVKMLRADANKNARNDFLKE IKIMSRLKDPNIIHLLSVCITDDPLCMITEYMENGDLNQFLSR HEPPNSSSSDVRTVSYTNLKFMATQIASGMKYLSSLNFVHRDL ATRNCLVGKNYTIKIADFGMSRNLYSGDYYRIQGRAVLPIRWM SWESILLGKFTTASDVWAFG\VTLWE\TFTFCQRKGPYS\QLS \DETGY*RNTGEFFPRPKGGQTYLPSTSPFVPDSCVIKLMLSC WRRDTKNRPSFQEIHLLLLQQGDERCCQCLAMFLRLRSSLQDL PLTHAYATPSGHLMKLRDRGLFALPSFPGHPHSLPLTHIYFFF
341	1080	916	3	CSASPLRPGLLAPDLLYLPGAGQPRRPEAEPGQKPVVPTLYVT EAEAHSPALPGLSGPQPKWVEVEETIEVRVKKMGPQGVSPTTE VPRSSSGHLFTLPGATPGGDPNSNNSNNKLLAQEAWAQGTAMV GVREPLVFRVDARGSVDWAASGMGSLEEEGTMEEAGEEEGEDG DAFVTEESQDTHSLGDRDPKILTHNGRMLTLADLEDYVPGEGE TFHCGGPGPGAPDDPPCEVSVIQREIGEPTVG\SLCCSAWGMH WVPEALSASLGLSPMGR\HHRDPRSVALRAPPSSCGRPRLGLW AVLPG
342	1081	862	444	QGLAAEFLQVPAVTRAYTAACVLTTAAVQLELLSPFQLYFNPH LVFRKFQAPFLPWALMGFSLLLGNSILVDLLGIAVGHIYYFLE DVFPNQPGGKRLLQTPGFLGLQSSKAPAGSSLTIWTQQSQGGP GTAGELAAPS

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
L	1082	sequence 3658	sequence	EKNALEPTVYFGMGV*APQVPRFQQRITGYQYYLQLRKDIWEE
343				GIPCTLEQPIHLAGLAVQAIFGDFDQYESQDFLQKFALFPVGW LQDEKVLEEATQKVALLHQKYRGLTAPDAEMLYMQEVERMDGY GEESYPAKDSQGSDISIGACLEGIFVKHKNGRHPVVFRWHDIA NMSHNKSFFALELANKEETIQFQTEDMETAKYIWRLCVARHKF YRLNQCNLQTQTVTVNPIRRRSSSRMSLPKPQPYVMPPPP\QL HYNGHYTEPYASSQDNLFVPNQEG\YYGQFQTSLNRAQIDFNG RIR\NASVYSAHSTNSLNNPQPYLQPSPMSSNPSITGSDVMRP DYLPSHRHSAVIPPSYRPTPDYETVMKQLNRGLVHAERQSHSL RNLNIGSSYAYSRPAALVYSQPEIREHAQLPSPAAAHCPFSLS YSFHSPSPYPYPAERRPVVGAVSVPELTNAQLQAQDYPSPNIM RTQVYRPPPPYPPPRPANSTPDLSRHLYISSSNPDLITRRVHH SVQTFQEDSLPVAHSLQEVSEPLTAARHAQLHKRNSIEVAGLS HGLEGLRLKERTLSASAAEV\APRAVSVGSQP\SVFTERTQRE GPEEAEGLRYGHKKSLSDATMLIHSSEEEEDEDFEEESGARAP PARAREPRPGLAQDPPGCPRVLLAGPLHILEPKAHVPDAEKRM MDSSPVRTTAEAQRPWRDGLLMPSMSESDLTTSGRYRARRDSL KKRPVSDLLSGKKNIVEGLPPLGGMKKTRVDAKKIGPLKLAAL NGLSLSRVPLPDEGKEVATRATNDERCKILEQRLEQGMVFTEY ERILKKRLVDGECSTARLPENAERNRFQDVLPYDDVRVELVPT KENNTGYINASHIKVSVSGIEWDYIATQGPLQNTCQDFWQMVW EQGIAIIAMVTAEEEGGREKSFRYWPRLGSRHNTVTYGRFKIT TRFRTDSGCYATTGLKMKHLLTGQERTVWHLQYTDWPEHGCPE DLKGFLSYLEEIQSVRRHTNSTSDPQSPNPPLLVHCSAGVGRT GVVILSEIMIACLEHNEVLDIPRVLDMLR\QQRMMLVQTLCQY TFVYRVLIQVPEKAPRLILSSPQFFYGAQSCEAFTA
344	1083	6	304	RKKQKLAEE*VELSKLADLKDAEAVQKFFLEEI*L\GEEILAK GVDHLTNPSAVCGQPQWLLQVLQQTLPLPVIQMLLTKPLPVNQ RLVSAG/SLAKDDVE
345	1084	1255	635	SFCLHEFGWLGSSPQSDHPVPALLGLGAFVHHSLLQVHSSPGA GPVSFLFLGESCSPVDEPRCVPSCAFGFLSCFPLLNSAALERG LFFFVVFFFLESGSCQVARAGVRD/RDRGSLQPPPPGLKQFCL SLPSRWDHRHPPPLRVP*FVFVFLVELGFHHVAQAGLKLLTLS DPPAPASHSAGITGVSQRDQPVLFLRWASCSELVG
346	1085	116	415	EGFPGRSLSGGLCCRLRRRFPIDGYRPRRRRRWSCCPSGVRPV RRMSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVR RGFTVLARMVSIS
347	1086	918	760	QNSTCLTAQTHSLLQHQPLQLTTLLDQYIREQREKDSVMSANG KPDPDTVPDS

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348	1087	1	750	LNPWKNALQDFCLPFLRITSLLQHHLFGEDLPSCQEEEEFSVL ASCLGLLPTFYQTEHPFISASCLDWPVPAFDIITHWCFEIKSF TERHAEQGKALLIQESKWKLPHLLQLPENYNTIFQYYHRKTCS VCTKVPKDPAVCLVCGTFVCLKGLCCKQQSYCECVLHSQNCGA GTGIFLLINASVIIIIRGHRFCLWGSVYLDAHGEEDRDLRRGK PLYICKERYKVLEQQWISHTFDHINKRWGPHYNGL
349	1088	3	1374	KGQLVNLLPPENFPWCGGSQGPRMLRTCYVLCSQAGPRSRGWQ SLSFDGGAFHLKGTGELTRALLVLRLCAWPPLVTHGLLLQAWS RRLLGSRLSGAFLRASVYGQFVAGETAEEVKGCVQQLRTLSLR PLLAVPTEEEPDSAAKSGEAWYEGNLGAMLRCVDLSRGLLEPP SLAEASLMQLKVTALTSTRLCKELASWVRRPGASLELSPERLA EAMDSGQNLQVSCLNAEQNQHLRASLSRLHRVAQYARAQHVRL LVDAEYTSLNPALSLLVAALAVRWNSPGEGGPWVWNTYQACLK DTFERLGRDAEAAHRAGLAFGVKLVRGAYLDKERAVAQL\HG\ MEDPPTQADYEATS\QSYS\RCLELMLTHVARHGPMCHLMVAS HNEESVRQATK\GQAGYVVYKSIPYGSLEEVIPYLIRRAQENR SVLQGARREQELLSQKLWRRLLPGCRRIPH
350	1089	1036	306	VVEFGEMSTARAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFK ALVITLDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYF QMTPISTSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHN VQGIIVSNHGGRQLDEVLASIDALTEVGAAE*GNMKYYLDAGV RTGNDVQKALALGAKCIFLGRPILWGLACKGEHGVKEVLNILT NEFHTSMA\LTGCRSVAEINRNLVQFSRL
351	1090	1229	957	FFLRWSFTL\LPRLE/CQWLNLGSLQPPPPGFK*SSCLRLLSS WGLQVPTSMLG*FFCIFSREGISPCWPGWSQTPKVIHLPRPPR VLRLQA
352	1091	1145	365	LLCFVHTALQSFQGELYEPHVVIAIVVFLVKLGICK*RASWRK KVTLVVK*S/LKICFTKYGSCYHPGEKSSSWLFN*RMVNDCLA TSCSNRSFVIQQIPSSNLFMVVVDSSCLCESVAPITMAPIEIR YILLCAGPLTTTETSKGYQW*GNLGEKY*RRKITSFPLLERES S*ESCHCQILTSEMQSRKKQSLETCLNYSQHNESLKCERLKAQ KIRRPESCHGFHPEENARECGGAPSLQAQTVLLLLPLLLMLF SR
353	1092	1140	790	VPSPTHDPKPAEAPMPA*PAPPGPASPGGALEPPAAARAGGSP TAVRSILTKERRPEGGYKAVWFGEDIGTEADVVVLNAPTLDVD GASDSGSGDEGEGAGRGGGPYDAPGGDDSYI

SEQ ID ID beginning nucleotide location of Mucleic Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acids Acid, E-Glutamic Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, K-Lysine, L-Leucine, M-Methionine, N-Asparagine, P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deleteration Acid Acids Acid, E-Glutamic Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Methionine, N-Asparagine, N-P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deleteration Acid Acids Acid Acid, E-Glutamic, Acid, E-Glutamic, Acid, E-Cysteine, D-Aspartic Acid, E-Glutamic, Acid, E-Cysteine, D-Aspartic Acid, E-Glutamic, Acid, E-Cysteine, D-Aspartic Acid, E-Glutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Phenylalanine, G-Glycine, H-Histidine, I-Isoleucine, M-Lutamic, Acid, E-Ph	<b>;</b> ,
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No:     of Nucleic Amino Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     Acids     A	
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Nucleic Acids Acids sponding to first amino acid residue of amino acid sequence sequence 354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	ion,
Acids to first amino acid residue of amino acid sequence sequence  354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	ion,
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acid residue of amino acid sequence  354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	,
residue of amino acid acid sequence sequence  354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	
of amino acid acid sequence sequence  354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	
acid acid sequence sequence  354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	1
Sequence   Sequence	
354 1093 3 2293 LISLAGPTDDIQSTGPQVHALNILRALFRDTRLGENIIPY GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	!
GAKAAILGFTSPVWAVRNSSTLLFSALITRIFGVKRAKDE TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	VAD
TNRMTGREFFSRFPELYPFLLKQLETVANTVDSDMGEPNR MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	HSK
MFLLLLVLERLYASPMDGTSSALSMGPFVPFIMRCGHSPV	
I I I I I I I I I I I I I I I I I I I	
REMARALVPFVMIDHIPNTIRTLLSTLPSCTDQCFRQNH	AVD
TLLQVFHLVQAYSDSKHGTNSDFQHELTDITVCTKAKLWL	EALED TOTAL
QNPCLVTRAVYIDILFLLTCCLNRSAKDNQPVLESLGFWE	
GIISGSELITGFPWAFKVPGLPQYLQSLTRLAIAAVWAAA	HAD
GERETNVPISFSQLLESAFPEVRSLTLEALLEKFLAAASG	
KGVPPLLCNMGEKFLLLAMKENHPECFCKILKILHCMDPG	
PQTEHCVHLTPKEFLIWTMDIASNERSEIQSVALRLASKV	
HMQTCVENRELIAAELKQWVQLVILSCEDHLPTESRLAVV	
TSTTPLFLTNPHPILELQDTLALWKCVLTLLQSEEQAVRD	
ETVTTAMSQENTCQSTEFAFCQVDASIALALALAVLCDLL	
DQLAPGLPILLGWLLGESDDLVACVESMHQVEEDYLFEKA	
FWAETLIFVKYLCKHLFCLLSKSGWRPPSPEMLCHLQRMV	SEQ
C\HLLSQFFRELPPAAEFVKTVEFTRLRIQEERTLACLRL	LAF
LEGKEGEDTLVLSVWDSYAESRQLTLPRTEAAC	
355 1094 25 1265 HAFRPIALQRGVSFRGCSNQYAESRRLQGESGSRAFAHLM	ESL
LQHLDRFSELLAVSSTTYVSTWDPATVRRALQWARYLRHI	HRR
FGRHGPIRTALERRLHNQWRQEGGFGRGPVPGLANFQALG	HCD
VLLSLRLLENRALGDAARYHLVQQLFPGPGVRDADEETLQ	ESL
ARLARRRSAVHMLRFNGYRENPNLQEDSLMKTQAELLLER	
VGKAEAERPARFLSSLWERLPQNNFLKVIAVALLQPPLSR	
EELEPGIHKSPGEGSQVLVHWLLGNSEVFAAFCRALPAGL	
VTSRHPALSPVYLGLLTDWGQRLHYDLQKGIWVGTESQDV	
ELHNRFQSLCQAPPPLKDKVLTALETCKAQDGDFEEPGLS	
DLLLALRSGAFRKRQVLGLSAGLSSV	
356 1095 3 . 1027 SHLIQHQRIHT*E*AHECNECGKAFSQTSCLIQHHKMHRK	EKS
YECNEYEGSFSHSSDLILQQEVLTRQKAFDCDVWEKNSSQ	
LVQHQSIHTKE/K/PHECNEDGKIF/NQIQA/LIQHLRVH	TRE
K\YVCTACGKAFSHSAIAQHQIIHTREKPSECDE*RKGI	SVK
LLIDSC/RIYTSEKSYKCIECGKFFMLLVFSYLSHIWRIF	
KFHCCNECEKAISQRNYLV+YQIHAMQKDYKCN/EACMCV	
SHNPTLIQHQRIYT*ENLFGCSK/C/GRSFNRSLTSLCHI	
I/RRQEFDVTQMEKLDTTFQA/STQHRNNGEKIVDYLFMK	ــــــــــــــــــــــــــــــــــــــ
HSPNLFHCTKI	
357 1096 2638 2867 AVTLTAKICSFTPEPSETMSPPAGTNNSRHAALRAVTLPV	KVC
SFTPEPARSRTHQKEETPNTSEHQKEQTPEAPP	

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  MAYSWQTDPNPNESHEKQYEHQEFLFVNQPHSSSQVSLGFDQI
358	1097	4747	4550	VDEISGKIPHYESEIDENTFFVPTAPKWDSTGHSLNEAHQISL NEFTSKSRELSWHQVSKAPAIGFSPSVLPKPQNTNKECSWGSP IGKHHGADDSRFSILAPSFTSLDKINLEKELENENHNYHIGFE SSIPPTNSSFSSDFMPKEENKRSGHVNIVEPSLMLLKGSLQPG MWESTWQKNIESIGCSIQLVEVPQSSNTSLASFCNKVKKIRER YHAADVNFNSGKIWSTTTAFPYQLFSKTKFNIHIFIDNSTQPL HFMPCANYLVKDLIAEILHFCTNDQLLPKDHILSVWGSEEFLQ NDHCLGSHKMFQKDKSVIQLHLQKSREAPGKLSRKHEEDHSQF YLNQLLEFMHIWKVSRQCLLTLIRKYDFHLKYLLKTQENVYNI IEEVKKICSVLGCVETKQITDAVNELSLILQRKGENFYQSSET SAKGLIEKVTTELSTSIYQLINVYCNSFYADFQPVNVPRCTSY LNPGLPSHLSFTVYAAHNIPETWVHRINFPLEIKSLPRESMLT VKLFGIACATNNANLLAWTCLPLFPKEKSILGSMLFSMTLQSE PPVEMITPGVWDVSQPSPVTLQIDFPATGWEYMKPDSEENRSN LEEPLKECIKHIARLSQKQTPLLLSEEKKRYLWFYRFYCNNEN CSLPLVLGSAPGWDERTVSEMHTILRRWTFSQPLEALGLLTSS FPDQEIRKVAVQQLDNLLNDELLEYLPQLVQAVKFEWNLESPL VQLLHRSLQSIQVAHRLYWLKNAENEAYFKSWYQKLLAALQ FCAGKALNDEFSKEQKLIKILGDIGERVKSASDHQRQEVLKKE IGRLEEFFQDVNTCHLPLNPALCIKGIDHDACSYFTSNALPLK ITFINANLMGKNISIIFKAGDDLRQDMLVLQLIQVMDNIWLQE GLDMQMIYRCLSTGKDQRLVQMVPDAVTLAKIHRHSGLIGPL KENTIKKWFSQHNHLKADYEKALRNFFYSCAGWCVVTFILGVC DRHNDNIMLTKSGHMFHIDFGKFLGHAQTFGGIKRDRAPFIFT SEM\EYFITEGG\KNPQHFQDFV\ELCCRAYNIIRKHSQLLL\ NLL\EMMLYAG\LPELSGI\QDLKYVYNNLRPQDTDLEATSHF TKKIKESLECFPVKLNNLIHTLAQMSAISPAKSTSQTFPQESC LLSTTRSIERATILGFSKKSSNLYLIQVTHSNNETSLTEKSFE QFSKLHSQLQKQFASLTLPEFPHWHLPFTNSDHRRFRDLNHY MEQILNVSHEVTNSDCVLSFFLSEAGQQTVEESSPVYLGEKFP DKKPKVQLVISYEDVKLTILVKHMKNIHLPDGSAPSAHVEFYL LPYPSEVRRRKTKSVPKCTDPTYNEIVVYDEVTELQGHVIMLI VKSKTVFVGAINIRLCSVPLDKEKWYPLGNSII*PLLLFYTSN FMQSVLH
359	1098	679	346	FFLRWSLDSVTQAGVQSHDLSSLQPPPPGFKQSSLFGLPSSWE *RWVPPCPANFFVFLVETGFRHVGQAGLELLTSNDLPVSACQS AGITGVTTVPQRKSMILYEVTICYP

SEQ ID ID NO: of of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
360 1099	2	1601	FVREIRGPAVPRLTSAEDRHRHGPHAHSPELQRTGRDYSLDYL PFRLWVGIWVATFCLVLVATEASVLVRYFTRFTEEGFCALISL IFIYDAVGKMLNLTHTYPIQKPGSSAYGCLCQYPGPGGNESQW IRTRPKDRDDIVSMDLGLINASLLPPPECTRQGGHPRGPGCHT VPDIAFFSLLLFLTSFFFAMALKCVKTSRFFPSVVRKGLSDFS SVLAILLGCGLDAFLGLATPKLMVPREFKPTLPGRGWLVSPFG ANPWWWSVAAALPALLLSILIFMDQQITAVILNRMEYRLQKGA GFHLDLFWVAVLMLLTSALGLPWYVSATVISLAHMDSLRRESR ACAPGERPNFLGIREQRLTGLVVFILTGASIFLAPVLKFIPMP VLYGIFLYMGVAALSSIQFTNRVKLLL\MPAKHQPDLLLLRHV PLTRVHLFTAISFA\CLGLLW\IIKSTPAAIIFPLMLLGLVGV RKALERVFSPQELLWLDELMPEEERSIPEKGLEPEHSFSGSDS EDSELMYQPKAPEINISVN*LE*EFVREIRGPAVPRLTSAEDR HRHGPHAHSPELQRTGRDYSLDYLPFRLWVGIWVATFCLVLVA TEASVLVRYFTRFTEEGFCALISLIFIYDAVGKMLNLTHTYPI QKPGSSAYGCLCQYPGPGGNESQWIRTRPKDRDDIVSMDLGLI NASLLPPPECTRQGGHPRGPGCHTVPDIAFFSLLLFLTSFFFA MALKCVKTSRFFPSVVRKGLSDFSSVLAILLGCGLDAFLGLAT PKLMVPREFKPTLPGRGWLVSPFGANPWWWSVAAALPALLLSI LIFMDQQITAVILNRMEYRLQKGAGFHLDLFCVAVLMLLTSAL GLPWYVSATVISLAHMDSLRRESRACAPGERPNFLGIREQRLT GLVVFILTGASIFLAPVLKFIPMPVLYGIFLYMGVAALSSIQF TNRVKLLLDASKTPARPATLAACASDQGPPLHSHQLCPVWGCF GIIKSTPAAIIFPLMLLGLVGVRKALERVFSPQELLWLDELMP EEERSIPEKGLEPEHSFSGSDSEDSELMYQPKAPEINISVN

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
361		1	2636	MGLKARRAAGAAGGGGDGGGGGGAANPAGGDAAAAGDEERKV GLAPGDVEQVTLALGAGADKDGTLLLEGGGRDEGQRRTPQGIG LLAKTPLSRPVKRNNAKYRRIQTLIYDALERPRGWALLYH\AL VFLIVLG\CLILAVL\TTFKEYETVSGDWLLLLETFAIFIFGA EFALRIWAAGCCCRYKGWRGRLKFARKPLCMLDIFVLIASVPV VAVGNQGNVLATSLRSLRFLQILRMLRDGPGEGGTWKLLG\SA ICAHSKELITAWYIGFLTLILSSFLVYLVEKDVPEVDAQGEEM KEEFETYADALWWGLITLATIGYGDKTPKTWEGRLIAATFSLI GVSFFALPAGILGSGLALKVQEQHRQKHFEKRRKPAAELIQAA WRYYATNPNRIDLVATWRFYESVVSFPFFRKEQLEAASSQKLG LLDRVRLSNPRGSNTKGKLFTPLNVDAIEESPSKEPKPVGLNN KERFRTAFRMKAYAFWQSSEDAGTGDPMAEDRGYGNDFPIEDM IPTLKAAIRAVRILQFRLYKKKFKETLRPYDVKDVIEQYSAGH LDMLSRIKYLQTRIDMIFTPGPPSTPKHKKSQKGSAFTFPSQQ SPRNEPYV\ARPST\SEI\EDQRH*WGKFVKSLKGQV\QGLGR KLDFLVDMHMQHMERLQVQVTEYYPTKGTSSPAEAEKKEDNRY SDLKTIICNYSETGPPEPPYSPHQVTIDKVSPYGFFAHDPVNL PRGGPSSGKVQATPPSSATTYVERPTVLPILTLLDSRVSCHSQ ADLQGPYSDRISPRQRRSITRDSDTPLSLMSVNHEELERSPSG FSISQDRDDYVFGPNGGSSWMREKRYLAEGETDTDTDPFTPSG SMP\LSSTGDGISDSVWTPSNKPI

SEQ ID ID NO: of Nucleic Acids Acids	Predicted beginning nucleotide location corre-	Predicted end nucleotide location	Amino acid segment containing signal peptide(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO: NO: of of Nucleic Amir	nucleotide location	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutainic Acid,
of of Nucleic Amir	location		
Nucleic Amin	COTTO		F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
1	_ COITE-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids Acid	0 1 '		P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	to first	to first	i = inreonine, v = vaime, w = fryptophian, i = i yrosine,
(	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	acid	acid	\=possible nucleotide insertion)
1	residue	residue	
	of amino	of amino	
İ	acid	acid	·
		sequence	
362 110	sequence	5433	RTRGIIEFDPKYTAFEVEEDVGLIMIPVVRLHGTYGYVTADFISQSSSASPGG
			VDYILHGSTVTFQHGQNLSFINISIIDDNESEFEEPIEILLTGATGGAVLGRH LVSRIIIAKSDSPFGVIRFLNQSKISIANPNSTMILSLVLERTGGLLGEIQVN WETVGPNSQEALLPQNRDIADPVSGLFYFGEGEGGVRTIILTIYPHESIEVEE TFIIKLHLVKGEAKLDSRAKDVTLTIQEFGDPNGVVQFAPETLSKKTYSEPLA LEGPLLITFFVRVKGTFGEIMVYWELSSEFDITEDFLSTSGFFTIADGESEA
	Ì	-	SFDVHLLPDEVPEIEEDYVIQLVSVEGGAELDLEKSITWFSVYANDDPHGVFA
1	ŀ		LYSDROSILIGONLIRSIOINITRLAGTFGDVAVGLRISSDHKEQRIVTENAE
	l l		ROLVVKDGATYKVDVVPIKNQVFLSLGSNFTLQLVTVMLVGGRFYGMPTILQE
1		1	AKSAVLPVSEKAANSOVGFESTAFOLMNITAGTSHVMISRRGTYGALSVAWTT
	Ì	1	GYAPGLEIPEFIVVGNMTPTLGSLSFSHGEQRKGVFLWTFPSPGWPEAFVLHL
	1	1	SGVQSSAPGGAQLRSGFIVAEIEPMGVFQFSTSSRNIIVSEDTQMIRLHVQRL
]	1	1	FGFHSDLIKVSYQTTAGSAKPLEDFEPVQNGELFFQKFQTEVDFEITIINDQL
	}	1	SEIEBFFYINLTSVEIRGLQKFDVNWSPRLNLDFSVAVITILDNDDLAGMDIS FPETTVAVAVDTTLIPVETESTTYLSTSKTTTILQPTNVVAIVTEATGVSAIP
1	1	1	EKLYTLHGTPAVSEKPDVATVTANVSIHGTFSLGPSIVYIEEEMKNGTFNTAE
	1	1	VLIRRTGGFTGNVSITVKTFGERCAQMEPNALPFRGIYGISNLTWAVEEEDFE
	1	[	EQTLTLIFLDGERERKVSVQILDDDEPEGQEFFYVFLTNPQGGAQIVEGKDDT
	į į		GFAAFAMVIITGSDLHNGIIGFSEESQSGLELREGAVMRRLHLIVTRQPNRAF
j	1	}	EDVKVFWRVTLNKTVVVLQKDGVNLMEELQSVSGTTTCTMGQTKCFISIELKP
) j	i	}	EKVPQVEVYFFVELYEATAGAAINNSARFAQIKILESDESQSLVYFSVGSRLA
			VAHKKATLISLQVARDSGTGLMMSVNFSTQELRSAETIGRTIISPAISGKDFV
	l l		ITEGTLVFEPGQRSTVLDVILTPETGSLNSFPKRFQIVLFDPKGGARIDKVYG
į	}	}	TANITLVSDADSQAIWGLADQLHQPVNDDILNRVLHTISMKVATENTDEQLSA
1	İ		MMHLIEKITTEGKIQAFSVASRTLFYEILCSLINPKRKDTRGFSHFAELTENF
	İ		AFSLLTNVTCGSPGEKSKTILDSCPYLSILALHWYPQQINGHKFEGKEGDYIR
l	1	ł	IPERLLDVQDAEIMAGKSTCKLVQFTEYSSQQWFISGNNLPTLKNKVLSLSVK
·	}	İ	GQSSQLLTNDNEVLYRIYAAEPRIIPQTSLCLLWNQAAASWLSDSQFCKVIEE TADYVECACLHMSVYAVYARTDNLSSYNBAFFTSGFICISGLCLAVLSHIFCA
1	i i		RYSMFAAKLLTHMMAASLGTQILFLASAYASPQLAEESCSAMAAVTHYLYLCQ
1	ı	1	FSWMLIQSVNFWYVLVMNDEHTERRYLLFFLLSWGLPAFVVILLIVILKGIYH
1 1	l l		QSMSQIYGLIHGDLCFIPNVYAALFTAALVPLTCLVVVFVVFIHAYQVKPQWK
1 1	1	Ì	AYDDVFRGRTNAAEIPLILYLFALISVTWLWGGLHMAYRHFWMLVLFVIFNSL
1	}	1	QLL\YPLFYFLLL*DQSSSASPGGVDYILHGSTVTFQHGQNLSFINISIIDDN
1	1	ļ	ESEFEEPIEILLTGATGGAVLGRHLVSRIIIAKSDSPFGVIRFLNQSKISIAN
1	1	ļ	PNSTMILSLVLERTGGLLGEIQVNWETVGPNSQEALLPQNRDIADPVSGLFYF
} }	}	1	GEGEGGVRTIILTIYPHEEIBVEETFIIKLHLVKGEAKLDSRAKDVTLTIQEF
i i	ì	1	GDPNGVVOFAPETLSKKTYSEPLALEGPLLITFFVRRVKGTFGEIMVYWELSS
1 1	i		EFDITEDFLSTSGFFTIADGESEASFDVHLLPDEVPEIEEDYVIQLVSVEGGA
( )	1	1	ELDLEKSITWFSVYANDDPHGVFALYSDRQSILIGQNLIRSIQINITRLAGTF
<b>!</b>	1	1	GDVAVGLRISSDHKEQPIVTENAERQLVVKDGATYKVDVVPIKNQVFLSLGSN
1 1	l l	1	FTLQLVTVMLVGGRFYGMPTILQEAKSAVLPVSEKAANSQVGFESTAFQLMNI
1		[	TAGTSHVMISRRGTYGALSVAWTTGYAPGLEIPEFIVVGNMTPTLGSLSFSHG
1	`\	1	EQRKGYFLWTFPSPGWPEAFVLHLSGVQSSAPGGAQLRSGFIVAEIEPMGVFQ FSTSSRNIIVSEDTQMIRLHVQRLFGFHSDLIKVSYQTTAGSAKPLEDFEPVQ
1. 1	}	1	FSTSSRNIIVSEDTQMIKLHVQKLFGFHSDLIKVSIQIIAGSAKFDBDFBFVQ NGELFFQKFQTEVDFEITIINDQLSEIEEFFYINLTSVEIRGLQKFDVNWSPR
1 1	1	1	NGELFFQKFQTEVDFETTIINDQLSEIEEFFIINLISVETKGLQKFDTMASTK LNLDFSVAVITILDNDDLAGMDISFPETTVAVAVDTTLIPVETESTTYLSTSK
1 1	1	1	TTTILQPTNVVAIVTEATGVSAIPEKLVTLHGTPAVSEKPDVATVTANVSIHG
	i	· ·	TFSLGPSIVYIEEEMKNGTPNTAEVLIRRTGGFTGNVSITVKTFGERCAQMEP
1	1	i	NALPFRGIYGISNLTWAVEEEDFEEQTLTLIFLDGERERKVSVQILDDDEPEG
1		}	OEFFYVFLTNPOGGAOIVEGKDDTGFAAFAMVIITGSDLHNGIIGFSEESQSG
, ]	1	ì	LELREGAVMRRLHLIVTROPNRAFEDVKVFWRVTLNKTVVVLQKDGVNLMEEL
1 1		ì	OSVSGTTTCTMGOTKCF1S1ELKPEKVPQVEVYFFVELYEATAGAAINNSARF
1	.	1	AOIKILESDESOSLVYFSVGSRLAVAHKKATLISLQVARDSGTGLMMSVNFST
	1	l	OELRSAETIGRTIISPAISGKDFVITEGTLVFEPGQRSTVLDVILTPETGSLN
	1	<b>\</b>	SFPKRFQIVLFDPKGGARIDKVYGTANITLVSDADSQAIWGLADQLHQPVNDD
	١	{	ILNRVLHTISMKVATENTDEQLSAMMHLIEKITTEGKIQAFSVASRTLFYEIL
1 1	1	1	CSLINPKRKDTRGFSHFAELTENFAFSLLTNVTCGSPGEKSKTILDSCPYLSI
1	ì	}	LALHWYPQQINGHKFEGKEGDYIRIPERLLDVQDAEIMAGKSTCKLVQFTEYS
1	l	1	SQQWFISGNNLPTLKNKVLSLSVKGQSSQLLTNDNEVLYRIYAAEPRIIPQTS
1	1	1	LCLLWNQAAASWLSDSQFCKVIEETADYVECACLHMSVYAVYARTDNLSSYNE
1		1	AFFTSGFICISGLCLAVLSHIFCARYSMFAAKLLTHMMAASLGTQILPLASAY
1	ļ	l	ASPQLAEESCSAMAAVTHYLYLCQFSWMLIQSVNFWYVLVMNDEHTERRYLLF FLLSWGLPAFVVILLIVILKGIYHQSMSQIYGLIHGDLCFIPNVYAALFTAAL
	1	ì	VPLTCLVVVFVVFIHAYQVKPQWKAYDDVFRGRTNAAEIPLILYLFALISVTW
1 1	ļ	l	LWGGLHMAYRHFWMLVLFVIFNSLQLLVPSVLLFTSMRSTFFSFHTGTLTSRE
j	İ	1	KKSTFVLTCLLSPDSKGLGVLCFLNTEWAFQVH
LL			TWO LEANT CHINGE DOUGHOATHE THE PRIME S

		<del></del>		in a signal postido (A = Ala-i-a
SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	<b>i</b>	acid	acid	\=possible nucleotide insertion)
	<b> </b> '	residue	residue	(-possible intelectine insertion)
	ļ	of amino	of amino	
	l	acid	acid	
		sequence	sequence	
363	1102	2	2855	AAGATMERDGCAGGGSRGGEGGRAPREGPAGNGRDRGRSHAAE
303	1102	~		APGDPQAAASLLAPMDVGEEPLEKAARARTAKDPNTYKVLSLV
1	ļ	[	1	LSVCVLTTILGCIFGLKPSCAKEVKSCKGRCFERTFG\NCRCD
ļ				AACVELG\NCCLGLPGGTCI\EP\EHIW\TCNKFRCG\EKRLT
1		1		RSLCACSDDCKD\RGDCLPSNLQFLCVQGE\KSWGRKNPCESH
1				LMEP\QCP\AGFETPSLPLLIF/SLDGFRAEYLHTWGGLLPVI
Į.				SKLKKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGIINNK
1	ļ		]	MYDPKMNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFF
1				WPGSDVEINGIFPDIYKMYNGSVPFEERILAVLQWLQLPKDER
	1	ł	ļ	WPGSDVEINGIPPDIIAMINGSVPFEERIDAVDQUDQDFADER
	1		ļ	PHFYTLYLEEPDSSGHSYGPVSSEVIKALQRVDGMVGMLMDGL
	ł			KELNLHRCLNLILISDHGMEQGSCKKYIYLNKYLGDVKNIKVI
l	1			YGPAARLRPSDVPDKYYSFNYEGIARNLSCREPNQHFKPYLKH
ł				FLPKRLHFAKSDRIEPLTFYLDPQWQLALNPSERKYCGSGFHG
İ		1	1	SDNVFSNMQALFVGYGPGFKHGIEADTFENIEVYNLMCDLLNL
1		1	ĺ	TPAPNNGTHGSLNHLLKNPVYTPKHPKEVHPLVQCPFTRNPRD.
			ł	NLGCSCNPSILPIEDFQTQFNLTVAEEKIIKHETLPYGRPRVL
	į		1	QKENTICLLSQHQFMSGYSQDILMPLWTSYTVDRNDSFSTEDF
1	1	1		SNCLYQDFRIPLSPVHKCSFYKNNTKVSYGFLSPPQLNKNSSG
	1	1	Į.	IYSEALLTTNIVPMYQSFQVIWRYFHDTLLRKYAEERNGVNVV
			Ī	SGPVFDFDYDG\RCDSL\ENLRQKRRVHPVTQENFWIPNSTSF
1			1	Y/VVLTSC\KDTSQTPLHC\ENL\DTLGFPFCLHRDWINSETC
1		(	1	\VHG\KHDSSW\VEEFVKCLHRA\RITGC*GTSLGLSFYQQRK
				EPVSDILKLKTHLPTFSQED
364	1103	657	1	TVPPPPGGPSPAPLHPKRSPTSTGEAELKEERLPGRKASCSTA
304	1100	00,	1 -	GSGSRGLPPL\SPMVSSAHNPNKAEIPERRKDSTSTPNNLPPS
				MMTRRNTYVCTERPGAERPSLLPNGKENSSGTPRVPPASPSSH
1		l	İ	SLAPPSGERSRLARGSTIRSTFHGGQVRDRRAGGWGWFFNKHA
	1	1	1	LORAPRNAGAPSLMPGHRTVLINYGGGQDLKNWETCLAAPPNK
	1	İ	ſ	HRR
L	<del> </del>	ļ. <u>.</u>	1333	HTLHHSSPTSEAEEFVSRLSTQNYFRSLPRGTSNMTYGTFNFL
365	1104	1	1313	GGRLMIPNTGISLLIPPDAIPRGKIYEIYLTLHKPEDVRLPLA
				GCOTLLSPIVSCGPPG\VLLTRPVILG\MDHCG\EPSPDSW\S
1				GCQTLLSPIVSCGPPG\VLLTRPVILG\PUMCG\EPSPDSW\S
	1	1		LRLKKQSCEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQL
	1			SRYALVGEALSVAAAKRLKLLLFAPVACTSLEYNILVYCLHDT
1	1			HDALNVVVQLEKQLQGQLIQEPLVLHFKDSYHNLRLSIHDVPS
	1	1		SLWKSKLLVSYQEIPFYHIWNGTQRYLHCTFTLERVSPSTSDL
1				ACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPAL
1	1		1	VGPSAFKIPFLIRQKIISSLDPPCRRGADWRTLAQKLHLDSHL
				SFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGTGPAGRW
1				LLSQCSEAEC
366	1105	1	343	GSAAGQVQQQQQRRHQQGKVTVKYDRKELRKRLVLEEWIVEQL
1		-		GOLYGCEEEMPEVEIDIDDLFDAYSDEQRASKLQEALVDCYK
1	1			PTEEFIKELLSRIRGMRKLSP\PQKKSV
1				

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning mucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
367	1106	sequence 2	1398	IMLDGRVRWLTPVISALWEAEMEDVIARMQDEKNGIPIRTVKS FLSKIPSVFSGSDIVQWLIKNLTIEDPVEALHLGTLMAAHGYF FPISDHVLTLKDDGTFYRFQTPYFWPSNCWEPENTDYAVYLCK RTMQNKARLELADYEAESLARLQRAFARKWEFIFMQAEAQAKV DKKRDKIERKILDSQERAFWDVHRPVPGCVNTTEVDIKKSSRM RNPHKTRKSVYGLQNDIRSHSPTHTPTPETKPPTEDELQQQIK YWQIQLDRHRLKMSKVADSLLSYTEQYLEYDPFLLPPDPSNPW LSDDTTFWELEASKEPSQQRVKRWGFGMDEALKDPVGREQFLK FLESEFSSENLRFWLAVEDLKKRPIKEVPSRVQEIWQEFLAPG APSAINLDSKSYDKTTQNVKEPGRYTFEDAQEHIYKLMKSDSY PRFIRSSAYQELLQAKK\KGKSLTSKRLTSLAQSY
368	1107	1	461	GTRDYPRIVNHLDHTYVTAPQAFMMFQYFVKVVPTVYMKVDGE VLTTNQIYVTRHEKAAYVLMGDQGLPGVFILYELSPMMVNLTE IHTFFSLFLTIVGA\TIGGMFFEHFVINYLTHKWGLGFYFKNE NSLQGGHRTLYGVNFFMYWSLRGGS
369	1108	2	1522	SVWWNSQRQFVVRAWGCAGPCGRAVFLAFGLGLGLIEEKQAES RRAVSACQEIQAIFTQKSKPGPDPLDTRRLQGFRLEEYLIGQS IGKGCSAAVYEATMPTLPQNLEVTKSTGLLPGRGPGTSAPGEG QERAPGAPAFPLAIKMMWNISAGSSSEAILNTMSQELVPASRV ALAGEYGAVTYRKSKRGPKQLAPHPNIIRVLRAFTSSVPLLPG ALVDYPDVLPSRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNT PSPRLAAMMLLQLLEGVDHLVQQGIAHRDLKSDNILVELDPDG CPWLVIADFGCCLADESIGLQLPFSSWYVDRGGNGCLMAPEVS TARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFYGQGKAHLE SRSYQEAQLPALPESVPPDVRQLVRALLQREASKRPSARVAAN VLHLSLWGEHILALKNIKLDKMVGWLLQQSAATLLANRLTEKC CVETKMKMLFLANLECETLCQAALLLCSWRAAL
370	1109	105	1252	RPLLRLAELPDHCYRMNSSPAGTPSPQPSRANGNINLGPSANP NAQPTDFDFLKVIGKGNYGKVLLAKRKSDGAFYAVKVLQKKSI LKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVLD YVNGGELFFHLQRERRFLEPRARFYAAEVASAIGYLHSLNIIY RDLKPENILLDCQGHVVLTDFGLCKEGVEPEDTTSTFCGTPEY LAPEVL\RKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVSQM YENILHQPLQIPGGRTVAACDLLQSLLHKDQRQRLGSKADFLE IKNHVFFSPINWDDLYHKRLTPPFNPNVTGPADLKHFDPEFTQ EAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDDILDC

050	CEC	Dundinted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ ID	Predicted beginning	end	Ammo acid segment containing signal peptide (A—Alamine,
ID NO:	NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	110.00	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
	1	residue	residue	
	1	of amino	of amino	
		acid	acid	
2.73	1110	sequence_	sequence 1608	RPOTLKGHQEKIRQRQSILPPPQGPAPIPFQHRGGDSPEAKNR
371	1110	] 3	1000	VGPQVPLSEPGFRRRESQEEPRAVLAQKIĘKETQILNCALDDI
		}		EWFVARLQKAAEAFKQLNQRKKGKKKGKKAPAEGVLTLRARPP
		ł		\SEGEFIDCFOKIKLAINLLAKLQKHIQNPSAAELVHFLFGPL
	ļ	!		DLIVNTCSGPDIARSVSCPLLSRDAVDFLRGHLVPKEMSLWES
	j		}	LGESWMRPRSEWPREPQVPLYVPKFHSGWEPPVDVLQEAPWEV
		1		EGLASAPIEEVSPVSRQSIRNSQKHSPTSEPTPPGDALPPVSS
			1	PHTHRGYQPTPAMAKYVKILYDFTARNANELSVLKDEVLEVLE
	i		ł	DGRQWWKLRSRSGQAGYVPCNILGEARPEDAGAPFEQAGQKYW
				GPASPTHKLPPSFPGNKDELMQHMDEVNDELIRKISNIRAQPQ
	1	İ		RHFRVERSQPVSQPLTYESGPDEVRAWLEAKAFSPRIVENLGI
	1	1		LTGPQLFSLNKEELKKVCGEEGVRVYSQLTMQKAFLEKQQSGS
	1			ELEELMNKFHSMNORRGEDS
372	1111	3	1046	AWHEGLVSSPAIGAYLSASYGDSLVVLVATVVALLDICFILVA
312	1111	١	1010	VPESLPEKMRPVSWGAQISWKQADPFASLKKVGKDSTVLL\IC
	1			ITVCLSYLPEAG\QYSSFF\LYLR\QVIGFG\SVKIAAFIAMV
ļ	İ	ŀ	]	GILSIVAQTAFLSILMRSLGNKNTVLLGLGFQMLQLAWYGFGS
	1	1		QAWMMWAAGTVAAMSSITFPAISALVSRNAESDQQGVAQGIIT
Ì	Ì			GIRGLCNGLGPALYGFIFYMFHVELTELGPKLNSNNVPLQGAV
1	]	ļ		IPGPPFLFGACIVLMSFLAALFIPEYSKASGVQKHSNSSSGSL
<u> </u>				TNTPERGSDEDIEPLLQDSSIWELSSFEEPGNQCTEL*TRQKV
				GFCIRHL
373	1112	1	1950	MAAGLATWLPFARAAAVGWLPLAQQPLPPAPGVKASRGDEVLV
	}	1	j	VNVSGRRFETWKNTLDRYPDTLLGSSEKEFFYDADSGEYFFDR
ļ			1	DPDMFRHVLNFYRTGRLHCPRQECIQAFDEELAFYGLVPELVG
]	1			DCCLEEYRDRKKENAERLAEDEEAEQAGDGPALPAGSSLRQRL
				WRAFENPHTSTAALVFYYVTGFFIAVSVIANVVETIPCRGSAR
]	]	]		RSSREQPCGERFPQAFFCMDTACVLIFTGEYLLRLFAAPSRCR
	1		1	FLRSVMSLIDVVAILPYYIGLLVPKNDDVSGAFVTLRVFRVFR
1				IFKFSRHSQGLRILGYTLKSCASELGFLLFSLTMAIIIFATVM
1	1		1	FYAEKGTNKTNFTSIPAAFWYTIVTMTTLGYGDMVPSTIAGKI
	1			FGSICSLSGVLVIALPVPVIVSNFSRIYHQNQRADKRRAQQKV
1	1	,		RLARIRLAKSGTTNAFLQYKQNGGLEDSGSGEEQAVCVRNRSA
1	1			FEQQHHHLLHCLEKTTCHEFTDELTFSEALGAVSPGGRTSRST
				SVSSQPVGPGSLLSSCCPRRAKRRAIRLANSTASVSRG\SMQE
				LDMLAGL\RRSHAP\QSRSSL\NAKPHDSLDLNCDSG\DFVAA
1	1			IISIPTPPANTPDESQPSSPGGGGRAGSTLRNSSLGTPCLFPE
				TVKISSL
374	1113	4	664	GWGKPFKDWTTGGQDTGGEPALLVGAGEGRAPRLNCPSGQIRS
1		I		PGPGDLSIYDNWIRYFNRSSPVYGLVP/RSKTSARIYPTYHTA
				FDTFDYVDKFLDPGEEGDKGHPETRTGEAED*ALALSPCRR\F
				SSHQAVARTAGSVILRLSDSFFLPLKVSDYSETLRSFLQAAQQ
			1	DLGALLEQHSISLGPLVTAVEKFEAEAAALGQRISTLQKGSPD
	1			PLQVRML



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning mucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
375	1114	1	1147	GIRGGGSLASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCF LLGVGCRLTPGLYHLGRTVLCIDFMVFTVRLLHIFTVNKQLGP KIVIVSKMMKDVFFFLFFLGVWLVAYGVATEGLLRPRDSDFPS ILRRVFYRPYLQIFGQIPQEDMDVALMEHSNCSSEPGFWAHPP GAQAGTCVSQYANWLVVLLLVIFLLVANILLVNLLIAMFSYTF GKVQGNSDLYWKAQRYRLIREFHSRPALAPPFIVISHLRLLLR QLCRRPRSPQPSSPALEHFRVYLSKEAERKLLTWESVHKENFL LARARDKRESDSERLKRTSQKVDLALKQLGHIREYEQRLKVLE REVQQCSRVLGWVAEALSRSALLPPGGPPPPDLPGSKD
376	1115	3	329	LIKLCKSKAKSCENDLEMGMLNSKFKKTRYQAGMRNSENLTAN NTLSKPTRY/QGELKEIKQDISSLRYELLEEKSQATGELADLI QQLSEKFGKNLNKDHLRVNKGKDI
377	1116	1	2043	LPLLHAGFNRRFMENSSIIACYNELIQIEHGEVRSQFKLRACN SVFTALDHCHEAIEITSDDHVIQYVNPAFERMMGYHKGELLGK ELADLPKSDKNRADLLDTINTCIKKGKEWQGVYYARRKSGDSI QQHVKITPVIGQGGKIRHFVSLKKLCCTTDNNKQIHKIHRDSG DNSQTEPHSFRYKNRRKESIDVKSISSRGSDAPSLQNRRYPSM ARIHSMTIEAPITKVINIINAAQENSPVTVAEALDRVLEILRT TELYSPQLGTKDEDPHTSDLVGGLMTDGLRRLSGNEYVFTKNV HQSHSHLAMPITINDVPPCISQLLDNEESWDFNIFELEAITHK RPLVYLGLKVFSRFGVCEFLNCSETTLRAWFQVIEANYHSSNA YHNSTHAADVLHATAFFLGKERVKGSLDQLDEVAALIAATVHD VDHPGRTNSFL\CNAGSELAVLYNDT\AV\LESHHTALAFQ\L TVKDTK\CNIFKNID/RGNHYRTLRQAIIDMVLATEMTKHFEH VNKFVNSINKPMAAEIEGSDCECNPAGKNFPENQILIKRMMIK CADVANPCRPLDLCIEWAGRISEEYFAQTDEEKRQGLPVVMPV FDRNTCSIPKSQISFIDYFITDMFDAWDAFAHLPALMQHLADN YKHWKTLDDLKCKSLRLPSDRLKPSHRGGLLTDKGHCESQ

SEQ ID ID ID NO: of of Amino Acids Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
378 1117	1	3585	AFLSKVEEDDYPSEELLEDENAINAKRSKEKNPGNQGRQFDVN LQVPDRAVLGTIHPDPEIEESKQETSMILDSEKTSETAAKGVN TGGREPNTMVEKERPLADKKAQRPFERSDFSDSIKIQTPELGE VFQNKDSDYLKNDNPEEHLKTSGLAGEPEGELSKEDHENTEKY MGTESQGSAAAEPEDDSFHWTPHTSVEPGHSDKREDLLIISSF FKEQQSLQRFQKYFNVHELEALLQEMSSKLKSAQQESLPYNME KVLDKVFRASESQILSIAEKMLDTRVAENRDLGMNENNIFEEA AVLDDIQDLIYFVRYKHSTAEETATLVMAPPLEEGLGGAMEEM QPLHEDNFSREKTAELNVQVPEEPTHLDQRVIGDTHASEVSQK PNTEKDLDPGPVTTEDTPMDAIDANKQPETAAEEPASVTPLEN AILLIYSFMFYLTKSLVATLPDDVQPGPDFYGLPWKPVFITAF LGIASFAIFLWRTVLVVKDRVYQVTEQQISEKLKTIMKENTEL VQKLSNYEQKIKESKKHVQETRKQNMILSDEAIKYKDKIKTLE KNQEILDDTAKNLRVMLESEREQNVKNQDLISENKKSIEKLKD VISMNASEFSEVQIALNEAKLSEEKVKSECHRVQEENARLKKK KEQLQQEIEDWSKLHAELSEQIKSFEKSQKDLEVALTHKDDNI NALTNCITQLNLLECESESEGQNKGGNDSDELANGEVGGDRNE KMKNQIKQMMDVSRTQTAISVVEEDLKLLQLKL\RASVSTKC\ NLEDQVKKLEDDRNSLQAAKAGLEDECKTLRQKVEILNELYQQ KEMALQKKLSQEEYERQEREHRLSAADEKAVSAAEEVKTYKRR IEEMEDELQKTERSFKNQIATHEKKAHENWLKARAAERAIAEE KREAANLRHKLLDLTQKMAMLQEEPVIVKPMPGKPNTQNPPRR GPLSQNGSFGPSPVSGGECSPPLTVEPPVRPLSATLNRRDMPR SEFGSLDGPLPHPRWSAEASGKPSPSDPGSGTATMMNSSSRGS SPTRVLDEGKVMMAPKGPPPFFGVPLMSTPMGGPVPPPIRYGP PPQLCGPFGPRPLPPPFGPGMRPPLGLREFAPGVPPGRRDLPL HPRGFLPGHAPFRPLGSLGPREYFIPGTRLPPPTHGPQEYPPP PAVRDLLPSGSRDEPPPASQSTSQDCSQALKQSP

SEQ ID NO:	SEQ ID NO:	Predicted beginning nucleotide	Predicted end nucleotide location	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	, possess amounts
		of amino	of amino	
		acid	acid	
		sequence	sequence	
379	1118	3	2946	MAADSEPESEVFEITDFTTASEWERFISKVEEVLNDWKLIGNS
				LGKPLEKGIFTSGTWEEKSDEISFADFKFSVTHHYLVQESTDK
			ļ	EGKDELLEDVVPQSMQDLLGMNNDFPPRAHCLVRWYGLREFVV
	Ì		1	IAPAAHSDAVLSESKCNLLLSSVSIALGNTGCQVPLFVQIHHK
			i	WRRMYVGECQGPGVRTDFEMVHLRKVPNQYTHLSGLLDIFKSK
				IGCPLTPLPPVSIAIRFTYVLQDWQQYFWPQQPPDIDALVGGE
				VGGLEFGKLPFGACEDPISELHLATTW\PHLTEGIIVDNDVYS DLDPIQAPHWSVRVRKAENPQCLLGDFVTEFFKICRRKESTDE
				ILGRSAFEEEGKETADITHALSKLTEPASVPIHKLSVSNMVHT
i		ļ		AKKKIRKHRGVEESPLNNDVLNTILLFLFPDAVSEKPLDGTTS
ĺ				TDNNNPPSESEDYNLYNOFKSAPSDSLTYKLALCLCMINFYHG
	l		1	GLKGVAHLWOEFVLEMRFRWENNFLIPGLASGPPDLRCCLLHQ
		}		KLOMINCCIERKKARDEGKKTSASDVTNIYPGDAGKAGDQLVP
	1	1		DNLKETDKEKGEVGKSWDSWSDSEEEFFECLSDTEELKGNGOE
İ		ł		SGKKGGPKEMANLRPEGRLYQHGKLTLLHNGEPLYIPVTQEPA
				PMTEDLLEEOSEVLAKLGTSAEGAHLRARMOSACLLSDMESFK
				AANPGCSLEDFVRWYSPRDYIEEEVIDEKGNVVLKGELSARMK
· .				IPSNMWVEAWETAKPIPARRORRLFDDTREAEKVLHYLAIQKP
ł		ľ		ADLARHLLPCVIHAAVLKVKEEESLENISSVKKIIKQIISHSS
ļ				KVLHFPNPEDKKLEEIIHQITNVEALIARARSLKAKFGTEKCE
			ļ	OEEEKEDLERFVSCLLEOPEVLVTGAGRGHAGRIIHKLFVNAQ
				RAAAMTPPEEELKRMGSPEERRONSVSDFPPPAGREFILRTTV
			1	PRPAPYSKALPORMYSVLTKEDFRLAGAFSSDTSFF
380	1119	2333	670	SPTRTGDRSVSLIVFLTEGKPTVGETHTLKILNNTREAARGQV
				CIFTIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGF
	ļ			YDEIRTPLLSDIRIDYPPSSVVQATKTLFPNYFNGSEIIIAGK
1	<u> </u>	ŀ		LVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTGSP
ļ		İ		RPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQ
	[		ļ	RAQALAVSYRFLTPFTSMKLRGPVPRMDGLEEAHGMSAAMGPE
			1	PVVQSVRGAGTQPGPLLKKPYQPRIKISKTSVDGDPHFVVDFP
				LSRLTVCFNIDGQPGDILRLVSDHRDSGVTVNGELIGAPAPPN
1	1.	1	1	GHKKQRTYLRTITILINKPERSYLEITPSRVILDGGDRLVLPC
		İ	1	NQSVVVGSWGLEVSVSANANVTVTIQGSIAFVILIHLYKKPAP
1	1	1		FQRHHLGFYIANSEGLSSNCHGLLGQFLNQDARLTEDPAGPSQ
	[			NLTHPLLLQVGEGPEAVLTVKGHQVPVVWKQRKIYNGEEQIDC
1				WFARNNAAKLIDGEYKDYLASHPFDTGMTLGQGMSREL
381	1120	102	426	VPLESLSCSHADNWKQELTKFISPDQLPVEFGGTMTDPDGNPK
1				CLTKINYGGEVPKSYYLCKQVRLQYEHTRSVGRGSSLQVENEI
				LFPGCVLRCPEVLQHLQPGSF

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
382	1121		3726	PAAPEHTDPSEPRGSVSCCSLLRGLSSGWSSPLLPAPVCNPNK AIFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSD SDVVEALSEEHMEADGHAAVVFGTVVDIISRSGEKIPVSVWMK RMRQERRLCCVVVLEPVERVSTWVAFQSDGTVTSCDSLFAHLH GYVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKIQRSVGRAR DGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISG LITLLPDGTIHGINHSFALTLFGYGKTELLGKNITFLIPGFYS YMDLAYNSSLQLPDLASCLDVGNESGCGERTLDPWQGQDPAEG GQDPRINVVLAGGHVVPRDEIRKLMESQDIFTGTQTELIAGGQ LLSCLSPQPAPGVDNVPEGSLPVHGEQALPKDQQITALGREEP VAIESPGQDLLGESRSEPVDVKPFASCEDSEAPVPAEDGGSDA GMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQLAGGS LLMHCPCYGSEWGLWWRSQDLAPSPSGMAGLSFGTPTLDEPWL GVENDREELQTCLIKEQLSQLSLAGALDVPHAELVPTECQAVT APVSSCDLGGRDLCGGCTGSSSACYALATDLPGGLEAVEAQEV DVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLAVGS DPDVGSLQEQGSCVLDDRELLLLTGTCVDLGQGRRFRESCVGH DPTEPLEVCLVSSEHYAASDRESPGHVPSTLDAGPEDTCPSAE EPRLNVQVTSTPVIVMRGAAGLQREIQEGAYSGSCYHRDGLRL SIQFEVRRVELQGPTPLFCCWLVKDLLHSQRDSAARTRLFLAS LPGSTHSTAAELTGPSLVEVLRARPWFEEPPKAVELEGLAACE GEYSQKYSTMSPLGSGAFGFVWTAVDKEKNKEVVVKFIKKEKV LEDCWIEDPKLGKVTLEIAILSRVEHANIIKVLDIFENQGFFQ LVMEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\QSRLV SAVGYLRLKDIIHRDIKDENIVIAEDFTIKLIDFGSAAYLERG KLFYTFCGTIEYCAPEVLMGNPYRGPELEMWSLGVTLYTLVFE ENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTL EKLVTDPWVTQPVNLADYTWEEVFRVNKPESGVLSAASLEMGN RSLSDVAQAQELCGGPVPGEAPNGQGCLHPGDPRLLTS
383	1122	177	1365	PGTSAATCRFLSPPVISLSFTGLCISDLVVAVNGVWILVETFM LKGGNFFSKHVPWSYLVFLTIYGVELFLKVAGLGPVEYLSSGW NLFDFSVTVFAFLGLLALALNMEPFYFIVVLRPLQLLRLFKLK ERYRNVLDTMFELLPRMASLGLTLLIFYYSFAIVGMEFFCGIV FPNCCNTSTVADAYRWRNHTVGNRTVVEEGYYYLNNFDNILNS FVTLFELTVVNNWYIIMEGVTSQTSHWSRLYFMTFYIVTMVVM TIIVAFILEAFVFRMNYSRKNQDSEVDGGITLEKEISKEELVA VLELYREARGASSDVTRLLETLSQMERYQQHSMVFLGRRSRTK SDLSLKMYQEEIQEWYEEHAREQEQQRQLSSSAAPAAQQPPGS RQRSQTVT

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	
NO:	NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	710105	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
i	ł	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	ļ	acid	acid	\=possible nucleotide insertion)
Į		residue	residue	,
Ì	1	of amino	of amino	
l		acid	acid	,
		sequence	sequence	
384	1123	1	986	LAGVGTQAPPRRPGGEMAAGQNGHEEWVGSAYLFVESSLDKVV
	}	l	ŀ	LSDAYAHPQQKVAVYRALQAALAESGGSPDVLQMLKIHRSDPQ
	l	1		LIVQLRFCGRQPCGRFLRAYREGALRAALQRSLAAALAQHSVP
]	ļ		ļ	LQL\DLRAGAERLEALLADEERCLSCILAQQPDRLRDEELAEL
	1	l		EDALRNLKCGSGARGGDGEVASAPLQPPVPSLSEVKPPPPPPP
1			Į	AQTFLFQGQPVVNRPLSLKDQQTFARSVGLKWRKVGRSLQRGC
	[			RALRDPALDSLAYEYEREGLYEQAFQLLRRFVQAEGRRATLOR
ļ	1	ļ		LVEALEENELTSLAEDLLGLTDPNGGLA
385	1124	2409	399	SSKPKLKKRFSLRSVGRSVRGSVRGILOWRGTVDPPSSAGPLE
			_	TSSGPPVLGGNSNSNSSGGAGTVGRGLVSDGTSPGERWTHRFE
	ł		]	RLRLSRGGGALKDGAGMVQREELLSFMGAEEAAPDPAGVGRGG
l	Ì		ł	GVAGPPSGGGGOPOWOKCRLLLRSEGEGGGGSRLEFFVPPKAS
		Į.		RPRLSIPCSSITDVRTTTALEMPDRENTFVVKVEGPSEYIMET
			į	VDAQHVKAWVSDIQECLSPGPCPATSPRPMTLPLAPGTSFLTR
			1	ENTDSLELSCLNHSESLPSODLLLGPSESNDRLSQGAYGGLSD
				RPSASISPSSASIAASHFDSMELLPPELPPRIPIEEGPPAGTV
	ŀ		j	HPLSAPYPPLDTPETATGSFLFQG\EPEGGEGDQPLSGYPWFH
'		1		GMLSRLKAAQLVLTGGTGSHGVFLVRQSETRRGEYVLTFNFQG
		ļ	1	KAKHLRLSLNEEGQCRVQHLWFQSIFDMLEHFRVHPIPLESGG
				SSDVVLVSYVPSSQRQQGEOSRSAGEEVPVHPRSEAGSRLGAM
1		1	Į.	RGCAREMDATPNASCTLMPFGASDC\EPTTSHDPPQPPEPPSW
	ţ			TDPPQPGEE\EASR\APGSGGQQAAAAAKERQEKEKAGG\GGV
	İ			PEE\LVPVV*LVPVGELGEGHRPQAQEAQGRLGPGGDAGVPP\
				1
205	1105	0004	1040	MVQLQQSPLGG\DGEEGGHPR\AI\NNQYSFV
386	1125	2204	1042	FRAPVGTAARSPQVVIRRLPPGLTKEQLEEQLRPLPAHDYFEF
	1		ŀ	FAADLSLYPHLYSRAYINFRNPDDILLFRDRFDGYIFLDSKDP
-			ļ	EYKKFLETYCVEEEKTSANPETLLGEMEAKTRELIARRTTPLL
				EYIKNRKLEKQRIREEKREERRRRELEKKRLREEEKRRRREEE
}	J			RCKKKETDKQKKIAEKEVRIKLLKKPEKGEEPTTEKPKERGEE
				IDTGGGKQESCAPGAVVKARPMEGSLEEPQETSHSGSDKEHRD
	1	]		VERSQEQESEAQRYHVDDGRRHRAHHEPERLSRRSEDEQRWGK
				GPGQDRGKKGSQDSGAPGEAMERLGRAQRCDDSPAPRKERLAN
<u></u>	<u></u>		<u></u>	KDRPALQLYDPGARFRARECGGNRRICKAEGSGTGPEKREEAE
387	1126	176	800	GVWGVCVSGLLQVGSQRAQAWRAWSPMETPLTGTFLWPHIPQG
	ł	1		LFFDDSYGFYPGQVLIGPAKIFSSVQWLSGVKPVLSTKSKFRV
	1			VVEEVQVVELKVTWITKSFCPGGTDSVSPP/PSVITQENLGRV
1	İ	1		KRLGCFDHAQR/HAWGALSVCLPSQGRASQDCLGMSRKKLRPG
		<b>]</b>		GGLYGQEGEAPVEEAGCADHVMLPRHPVFPGPFHGRPR
		<u> </u>	<del></del>	<u> </u>

OFC 1	erc	Dandi	Daidiana	TATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
SEQ	SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of Nucleic	of Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion.
1 1	1	acid	acid	\=possible nucleotide insertion)
		residue	residue	Tobbiolo national institution,
		of amino	of amino	
		acid	acid	,
	:	sequence	sequence	
388	1127	1	2017	FRDSSPCSAFEFHCLSGECIHSSWRCDGGPDCKDKSDEENCAV
				ATCRPDEFQCSDGNCIHGSRQCDREYDCKDMSDEVGCVNVTLC
				EGPNKFKCHSGECITLDKVCNMARDCRDWSDEPIKECGTNECL
				DNNGGCSHVCNDLKIGYECLCPDGFQLVAQRRCEDIDECQDPD
				TCSQLCVNLEGGYKCQCEEGFQLDPHTKACKAVGSIAYLFFTN
				RHEVRKMTLDRSEYTSLIPNLRNVVALDTEVASNRIYWSDLSQ
				RMICSTQLDRAHGVSSYDTVISRDIQAPDGLAVDWIHSNIYWT
				DSVLGTVSVADTKGVKRKTLFRENGSKPRAIVVDPVHGFMYWT
				DWGTPAKIKKGGLNGVDIYSLVTENIQWPNGITLDLLSGRLYW
i i				VDSKLHSISSIDVNGGNRKTILEDEKRLAHPFSLAVFEDKVFW
				TDIINEAIFSANRLTGSDVNLLAENLLSPEDMVLFHNLTQPRG
				VNWCERTTLSNGGCQYLCLPAPQINPHSPKFTCACPDGMLLAR
				DMRSCLTEG\EAAVATOETSTVRLKVSSTAVRTOHTTTRPVPD
				TSRLPGATPGLTTVEIVTMSHQALGDVAG\RGN\EKKPSSVRA
				LSIVLPIV\LLVFLCLGVFLLWKNWRLKNINSINFDNPVYQKT
				TEDEVHICHNODGYSYPSROMVSLEDDVA
389	1128	2299	1148	RIPGLGPPGSPPPPPHVRGMPGCPCPGCGMAGPRLLFLTALAL
				ELLGRAGGSQPALRSRGTATACRLDNKESESWGALLSGERLDT
				WICSLLGSLMVGLSGVFPLLVIPLEMGTMLRSEAGAWRLKOLL
]				SFALGGLLGNVFLHLLPEAWAYTCSASPGGEGQSLQQQQOLGL
1				WVIAGILTFLALEKMFLDSKEEGTSOAPNKDPTAAAAALNGGH
				CLAOPAAEPGLGAVVRSIKVSGYLNLLANTIDNFTHGLAVAAS
				FLVSKKIGLLTTMAILLHEIPHEVGDFAILLRAGFDRWSAAKL
			•	QLSTALGGLLGAGFAICTQSPKGVEETAAWVLPFTSGGFLYIA
	İ			LVNVLPDLLEEEDPWRSLQQLLLLCAGIVVMVLFSLFVD
390	1129	ī	523	GKVSAGQAGADRTLRRAPEPRFSQEPTGNSAYPQLRPFLDPQG
		-		RDLKPSALVPPTRSHTGRRPWLHTOPLPGPOGRAWGPTC/TPA
				CVDRVLESEEGRREYLAFPTSKSSGQKGRKELLKGNGRRIDYM
]		1		LHAEEGLCPDWKAEVEEFSFITOLSGLTDHLPVAMRLMVSSGE
				EEA
391	1130	1459	765	PCGGIRLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGS
			'''	AVIKFCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPE
				GHLNLTAPCNAACSCOPEHYSPVCGSDGLMYFSLCHAGCPAAT
	1			ETNVDGQKVSGAAAYRPCPPLDPGKGPPCLPLVIGAIVGLPRC
		İ		TETVAVSLRIFPLVLAM\HCREMHFNLSEKAPPSGFHIRCNFL
		1		YIPOOHSCTNGNSTMCP
392	1131	1668	962	LLRKVGAPGGARGVIRLLDWFERPDGFLLVLERPEPA\QD\LF
374	1131	1008	702	DFITERGALDEPLARRF\FAQVLAAVRHCHSCGVVHRDIKDEN
				LLVDLRSGELKLIDFGSGALLKDTVYTDFDGTRVYSPPEWIRY
	İ			HRYHGRSATVWSLGVLLYDMVCGDIPFEQDEEILRGRLLFRRR
		[	1	VSPECQQLIRWCLSLRPSERPSLDQIAAHPWMLGADGGAPESC
		<u> </u>	<u> </u>	DLRLCTLDPDDVASTTSSSESL

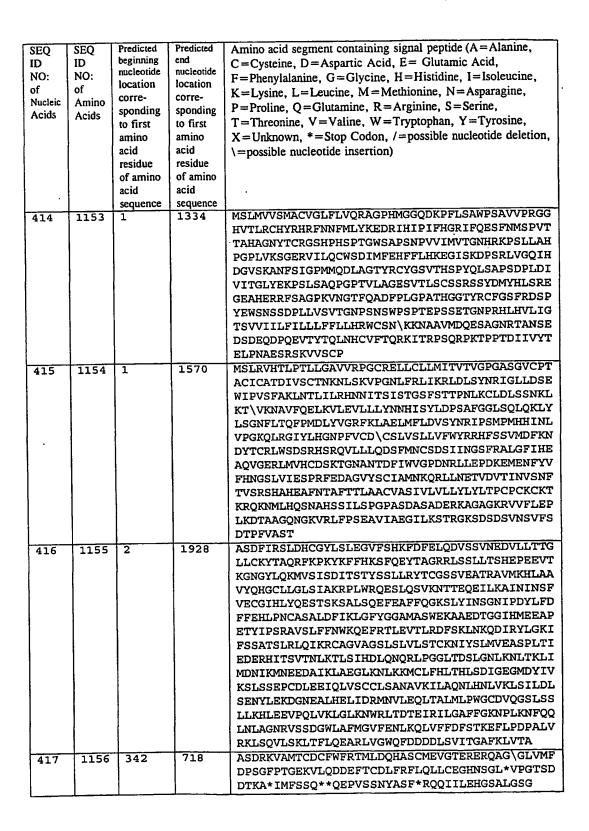
SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A = Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	согге-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	, , possissi ilaviouria ilaviouria,
ł	į	of amino	of amino	
	]	acid	acid	
ļ		sequence	sequence	
393	1132	3	817	GKNSQKASPVDDEQLSVCLSGFLDEVMKKYGSLVPLSEKEVLG
}		1	ļ	RLKDVFNEDFSNRKPFINREITNYRARHQKCNFRIFYNKHMLD
]	i	}	1	MDDLATLDGQNWLNDQVINMYGELIMDAVPDKVHFFNSFFHRQ
1	Ì		Į.	LVTKGYNGVKRWTKKVDLFKKSLLLIPIHLEVHWSLITVTLSN
	Į.	Ì	1	RIISFYDSQGIHFKFCVENIRKYLLTEAREKNR\LNLQGWQTA
	ļ	1		VTKCIPQQKNDSDCGVFVLQYCKCLAL\KQPFQFSQEDMPRVR
		1	1	KRIYKELCECRLMD
394	1133	1252	628	PPGG*QGSAAKHR/FP/KGYRHPALEARLGRRRTVQEARALLR
33.5		1		CRRAGISAPVVFFVDYASNCLYMEEIEGSVTVRDYIQSTMETE
	Ì		i	K\TPOGLSNLAKTIGOVLARMHDEDLIHGDLTTSNMLLKPPLE
	ļ	İ		OLNIVLIDEGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVF
	1	1	}	EAFLKSYSTSSKKARPVLKKLDEVRLRGKKRSMVG
395	1134	2	1595	RACVFRPEDMMQGEAHPSASLIDRTIKMRKETEARKVVLAWGL
393	1134	*	1333	LNVSMAGMIYTEMTGKLISSYYNVTYWPLWYIELALASLFSLN
}	Į.		1	ALFDFWRYFKYTVAPTSLVVSPGQQTLLGLKTAVVQTTPPHDL
l			ļ	AATQIPPAPPSPSIQGQSVLSYSPSRSPSTSPKFTTSCMTGYS
		ļ	}	POLOGLSSGGSGSYSPGVTYSPVSGYNKLASFSPSPPSPYPTT
1 '		İ	•	VGPVESSGLRSRYRSSPTVYNSPTDKEDYMTDLRTLDTFLRSE
				EEKQHRVKLGSPDSTSPSSSPTFWNYSRSMGDYAQTLKKFQYQ
				LACRSOAPCANKDEADLSSKQAAEEVWARVAMNRQLLDHMDSW
1	1	1	İ	TAKFRNWINETILVPLVQEIESVSTQMRRMGCPELQIGEASIT
	į	ļ		SLKOAALVKAPLIPTLNTIVQYLDLTPNQEYLFERIKELSQGG
	İ		1	CMSSFRWNRGGDFKGRKWDTDLPTDSAIIMHVFCTYLDSRLPP
	1		1	HPKYPDGKTFTSQHFVQTPNKPDVTNENVFCIYQSAINPPHYE
1	1			I I
<u> </u>	1		1540	LIYQRHVYIPAKGQK SSAVEFINRNNSVVQVLLAAGADPNLGDDFSSVYKTAKEQGIH
396	1135	16	1542	
				SLEVLITREDDFNNRLNNRASFKGCTALHYAVLADDYRTVKEL
ł				LDGGANPLQRNEMGHTPLDYAREGEVMKLLRTSEAKYQEKQRK
				REAEERRRFPLEQRLKEHIIGQESAIATVGAAIRRKENGWYDE
	1	1		EHPLVFLFLGSSGIGKTELAKQTAKYMHKDAKKGFIRLDMSEF
				QERHEVAKFIGSPPGYVGHEEGGQLTKKLKQCPNAVVLFDEVD
				KAHPDVLTIMLQLFDEGRLTDGKGKTIDCKDAIFIMTSNVASD
				EIAQHALQLRQEALEMSRNRIAENLGDVQISDKITISKNFKEN
				VIRPILKAHFRRDEFLGRINEIVYFLPFCHSELIQLVNKELNF
				WAKRAKQRHNITLLWDREVADVLVDGYNVHYGARSIKHEVERR
	1		ļ	VGNQLAAAYEQDLLP\GGCTLRITVEDSDKQLLKSPELPSPQA
1		1		EKRLPKLRLEIIDKDSKTRRLDIRAPLHPEKVCNTI
397	1136	1848	1602	SSCDRERHGSLGMMSGSFILCLALVTRWSPQASSVPLAVYESK
1	ļ			TRKSYRSQRDRDGKDRSQGMGLSLLVETRKLLLSANQG
		<del> </del>		

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
398	1137	1497	717	HTPMA/FFL/SFLSTSET/VYTFVILPKMLINLLSVARTISFN CCALQMFFFLGFAITNCLLLGVMGYDRYAAICHPLHYPTLMSW QVCGKLAAACAIGGFLASLTVVNLVFSLPFCSTNKVNHYFCDI SAVILLACTNTDVNGFVIFICGVLVLVVPFLFICVSYFCILRT ILKIPSAEGRRKAFSTCASHLSVVIVHYGCASFIYLRPTANYV SNKDRLVTVTYTIVTPLLNPMVYSLRNKDVQLAIRKVLGKKGS LKLYN
399	1138	2	1185	RPPAATRYPREKLKSMTSRDNYKAGSREAA\AAAAAVAAAAA AAAAEPYPVSGAKRKYLEDSDPERSDYEEQQLQEEEEARKVK SGIRQMRLFSQDECAKIEARIDEVVSRAEKGLYNEHTVDRAPL RNKYFFGEGYTYGAQLQKRGPGQERLYPPGDVDEIPEWVHQLV IQKLVEHRVIPEGFVNSAVINDYQPGGCIVSHVDPIHIFERPI VSVSFFSDSALCFGCKFQFKPIRVSEPVLSLPVRRGSVTVLSG YAADEITHCIRPQDIKERRAVIILRKTRLDAPRLETKSLSSSV LPPSYASDRLSGNNRDPALKPKRSHRKADPDAAHRPRILEMDK EENRRSVLLPTHRRRGSFSSENYWRKSYESSEDCSEAAGSPAR KVKMRRH
400	1139	60	1699	VTWHFYFCSDHKNGHYIIPQMADRSRQKCMSQSLDLSELAKAA KKKLQALSNRLFEELAMDVYDEVDRRENDAVWLATQNHSTLVT ERSAVPFLPVNPEYSATRNQGRQKLARFNAREFATLIIDILSE AKRRQQGKSLSSPTDNLELSLRSQSDLDDQHDYDSVASDEDTD QEPLRSTGATRSNRARSMDSSDLSDGAVT\LQEYLELKKALAT SEAKVQQLMKVNSSLSDEL\RRLQREHFAPI\IHKLQAENLQL RQPPGPVPTPPLPSERAEHTPMAPGGSTHRRDRQAFSMYEPGS ALKPFGGPPGDELTTRLQPFHSTELEDDAIYSVHVPAGLYRIR KGVSASAVPFTPSSPLLSCSQEGSRHTSKLSRHGSGADSDYEN TQSGDPLLGLEGKRFLELGKEEDFHPELESLDGDLDPGLPSTE DVILKTEQVTKNIQELLRAAQEFKHDSFVPCSEKIHLAVTEMA SLFPKRPALEPVRSSLRLLNASAYRLQSECRKTVPPEPGAPVD FQLLTQQVIQCAYDIAKAAKQLVTITTREKKQ

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	ŀ	acid	acid	\=possible nucleotide insertion)
		residue	residue	1—possible flucteoffide insertion)
ļ		of amino	of amino	
		acid	acid	
ļ	1	sequence	sequence	i i
401	1140	1	1863	RYLSYGSGPKRFPLVDVLQYALEFASSKPVCTSPVDDIDASSP
301		-		PSGSIPSQTLPSTTEQQGALSSELPSTSPSSVAAISSRSVIHK
				PFTQSRIPPDLPMHPAPRHITEEELSVLESCLHRWRTEIENDT
	İ		1	RDLOESISRIHRTIELMYSDKSMIQVPYRLHAVLVHEGQANAG
İ		}		HYWAYIFDHRESRWMKYNDIAVTKSSWEELVRDSFGGYRNASA
1	1	1	1	YCLMYINDKAQFLIQEEFN/K/ETGQPLVGIETLPPDLRDFVE
1	1			EDNORFEKELEEWDAQLAQKALQEKLLASQKLRESETSVTTAQ
			1	AAGDPKYLEQPSRSDFSKHLKEETIQIITKASHEHEDKSPETV
			1	LOSAIKLEYARLVKLAQEDTPPETDYRLHHVVVYFIQNQAPKK
1		1		IIEKTLLEOFGDRNLSFDERCHNIMKVAQAKLEMIKPEEVNLE
		İ	· ·	EYEEWHODYRKFRETTMYLIIGLENFQRESYIDSLLFLICAYQ
1	1			NNKELLSKGLYRGHDEELISHYRRECLLKLNEQAAELFESGED
'		1	1	
				REVNNGLIMNEFIVPFLPLLLVDEMEEKDILAVEDMRNRWCS
			į.	YLGQEMEPHLQEKLTDFLPKLLDCSMEIKSFHEPPKLPSYSTH
į.	1		1	ELCERFARIMLSLSRTPADGR
			<del></del>	THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P
402	1141	1	465	AQVYVRMDSFDEDLARPSGLLAQERKLCRDLVHSNKKEQEFRS
402	1141	1	465	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH
402	1141	1	465	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA
402				IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY
402	1141	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC
,				IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET
,			369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN
,				IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE ASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE ASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE KDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICG
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE ASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE KDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICG ASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE ASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE KDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICG ASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVR
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE ASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE KDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICG ASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVR PICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVI
403	1142	2	369	IFQHIQSAQSQRSPSELFAQHM\VPIVHHVKEHHFGSSGMTLH ERFT\KYLKRG\TEQEAAKNKKSPEIHRRIDISPSTFRKHGLA HDEMKSPREPGYKDGHNSKNELQRVNFY  TYTFCFSLMI\ILLTIIQGLILEAFGELRDQLDQVKEDMETKC FICGIGNDYFDTVPHGFETHTLQEHNLANYLFFLMYLINKDET EHTGQESYVWKMYQERCWEFFPAGDCFRKQYEDQLN  FRRKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKV EKHGPGRWVVLAAVLIGLLLVLLGIGFLVWHLQYRDVRVQKVF NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPF LGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEE RVVMLPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNSCSFGLH ARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRS FDLASCDERGRHLV\TVYNT\LSPMEPHA\LVQLCGTYPPSYN LTFHS\S\QNVLLITLITNTERRHPG\FEATFFQLPRMSSCGG RLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRFKFF YLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVR FHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRC DGWADCTDHSDELNCSCDAGHQFTCKNKFCKPLFWVCDSLNDC GDNSDEQGCSCP\AQTFRCSNGKCLSKSQQCNGKDDCGDGSDE ASCPKVNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE KDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICG ASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRS APGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVR

CEO I	ero.	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ ID	beginning	end	Annino acid segment containing signal populae (A - Alanine,
ID NO:	NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
710103	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	,	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	•
		of amino	of amino	,
	1	acid	acid	
		sequence	sequence	
405	1144	1	424	RHEEDLGNLWENTRFTDCSFFVRGQEFKAHKSVLAARSPVFNA
		ļ		MFEHEMEESKKNRVEINDLDPEVFKEMMRFIYTGRAPNLDKMA
			•	DNLLAAADKYALERLKVMCEKALCSNLSVENVADTLVLADLHS
				\AEQLKAQAIDFINRCSVLRQLGCKDGKNWNSNQATDIMETSG
			1	GKSMIQSHPHLVAEAFRALASAQGPQFGIPRKRLKQS*NLGNL
				WENTRFTDCSFFVRGQEFKAHKSVLAARSPVFNAMFEHEMEES
	1	į.	l	KKNRVEINDLDPEVFKEMMRFIYTGRAPNLDKMADNLLAAADK
			•	YALERLKVMCEKALCSNLSVENVADTLVLADLHSGRTVESTSH
				RLY
406	1145	1	1021	QRGGIPGKFQEDSGSVDWALGPFWGIFQADFGCMRFYLSAQTS
				DPVLRM*WGPSPISHPTSLCPGGGGAGQTTGSLCLGQQCCPLS
		1		CPNIPSRHKRWRL*AALVAGSRGSCTLRS*R*RTPLPVTRNLP
		ļ	ļ	R/CHLHLHPTGDLRVHVHQHCLLHGHVPPGAALLQCGGCDLRG
			ì	EAAGLLFLGHACLRGSVNLRRDQWLPV\PYSRLCFSGAREGHL
		1		PSLLAMIHVRHCTPIPALLVC\PIKVNLLIPVAYLVFWAFLLV
	ĺ		ļ	FSFISEHMVCGVGVIIILTGVPIFFLGVFWRSKPKCVHRLTES
	ļ		1	MTHWGQELCFVVYPQDAPEEEENGPCPPSLLPATDKPSKPQ
407	1146	2	1280	AAALVAEYLALLEDHRHLPVGCVSFQNISSNVLEESAISDDIL
		1 -		SPDEEGFCSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYK
İ	1	1		NLIPILEAHRDYKKLAAVHGKLQEAFTKIMHQSSGWERVFGTY
ļ	1	1	Į	FRVGFYGAHFGDLDEOEFVYKEPSITKLAEISHRLEEFYTERF
			1	GDDVVEIIKDSNPVDKSKLDSQKAYIQITYVEPYFDTYELKDR
		1	1	VTYFDRNYGLRTFLFCTPFTPDGRAHGELPEQHKRKTLLSTDH
	İ	1		AFPYIKTRIRVCHREETVLTP\VEVAIEDMQKKTRELAFATEQ
ļ				DPPDAKMLOMVLOGSVGPTVNQGPLEVAQVFLAEIPEDPKLFR
		1		HHNKLRLCFKDF*KKCEDALRKNKALIGPDQKEYHRELERNY
	1			CRLREALQPLLTQRLPQLMAPTPPGLRNSLNRASFRKADL
408	1147	55	651	GEGOOWOSTPLSPLOPTVADFLNLAWWTSAAAW*VLSGRWVEK
300	/	"		VLPGREGSEEK*GMASSSADHLHSAPRALQ\SLFQQLLYGLIY
	1			HSWFOAGR*GFGGASSSPGPQSELRRLHGEGGVYD*GRPETLP
	1			GSVGGAEALWALADPAEAEGSPETRESSCVMKQTQYYFGSVNA
			į	SYNAIIDCGNCSRCWQWGGTRGQGRNL
409	1148	1855	904	VAGIPACFDN/FTEALAETACROMGYSSKPTFRAVEIGPDQDL
409	1749	1033	304	DVVEITENSQELRMRNSSGPCLSGSLVSLHCLACGESLKTPRV
			1	VGGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFR
				KHTDVFNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMYPKDNDI
				ALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWGFTKQ
				NGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
1				GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYT
L	<u></u>		<u> </u>	KVSAYLNWIYNVWKAEL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
410	1149	3	964	TISTVRWNSRIGMVLGVAIQKRAV\PGLY\AFEEAYARADKEA PRPCHKGSWCSSNQLCRECQAFMAHTMPKLKAFSMSSAYNAYR AVYAVAHGLHQLLGCASGACSRGRVYPWQLLEQIHKVHFLLHK DTVAFNDNRDPLSSYNIIAWDWNGPKWTFTVLGSSTWSPVQLN INETKIQWHGKDNQVPKSVCSSDCLEGHQRVVTGFHHCCFECV PCGAGTFLNKS/SYLGKDLPENYNEAKCVTFSLLFNFVSWIAF FTTASVYDGKYLPAANMMAGLSSLSSGFGGYFLPKCYVILCRP DLNSTEHFQASIQDYTRRCGST
411	1150	2	1378	VARGAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQD ATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQ AEAQKVTFSQDPTTVALCISKEGRPPARISWLSSLDWEAKETQ VSGTLAGTVTVTSRFTLVPSGRADGVTVTCKVEHESFEEPALI PVTLSVRYPPEVSISGYDDNWYLGRTDATLSCDVRSNPEPTGY DWSTTSGTFPTSAVAQGSQLVIHAVDSLFNTTFVCTVTNAVGM GRAEQVIFVRETPNTAGAGATGGIIGGIIAAIIATADA\TGIL ICRQQRKEQTLQGABEDEDLEGPPSYKPPTPKAKLEAQEMPSQ LFTLGASEHSPLKTPYFDAGASCTEQEMPRYHELPTLEERSGP LHPGATSLGSPIPVPPGPPAVEDVSLDLEDEEGEEEEYLDKI NPIYDALSYSSPSDSYQGKGFVMSRAMYV
412	1151	1	1828	GTRLREDKNHNMYVAGCTEVEVKSTEEAFEVFWRGQKKRRIAN THLNRESSRSHSVFNIKLVQAPLDADGDNVLQEKEQITISQLS LVDLAGSERTNRTRAEGNRLREAGNINQSLMTLRTCMDVLREN QMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMIVCVNPKAEDY EENLQVMRFAEVTQEVEVARPVDKAICGLTPGRRYRNQPRGP\ IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRLIEALEKRH NLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQGKLNEKE KMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEEDKRNLQQ ELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKECERRVA AKQLEMQNKLWVKDEKLKQLKAIVTEPKTEKPERPSRERDREK VTQRSVSPSPVPLLFQPDQNAPPIRLRHRRSRSAGDRWVDHKP ASNMQTETVMQPHVPHAITVSVANEKALAKCEKYMLTHQELAS DGEIETKLIKGDIYKTRGGGQSVQFTDIETLKQESPNGSRKRR SSTVAPAQPDGAESEWTDVETRCSVAVEMRAGSQLGPGYQHHA QPKRKKP
413	1152	1	336	PFSSSSVSKGSDPFGTLDPFGSGSFNSAEGFADFSQMS/KGK STPVSQLGSADFPEAPDPFQPLGADSGDPFQSKKGFGDPFSGK DPFVPSSAAKPSKASASGFADFTSVS



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
418	1157	1	135	EITHIVGETAAFLCPRLRIRRGGKDGSPKPGFLASVIPVDRRP GE*DITHIVGETAAFLCPRLRIRRGGKDGSPKPGFLASVIPVD RRPGE
419	1158	173	943	SKFIFYVDSQSMIFFFQTPTRHKVLIMEFCPCGSLYTVLEEPS NAYGLPESEFLIVLRDVVGGMNHLRENGIVHRDIKPGNIMRVI GEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYLHPDMYERA VLRKDHQ\KKYGAT\VDLW\SIGVTFYQGKPTGS\LAI*HPFE GASVRNKASDGIKIITGKGLLGAIS\GVQKSKKNG\PI\DWEW EDMPVSCSPSSGVLRVPNLPPVLA\NILESRSRKKCWGF*PSF LQEN
420	1159	987	500	GSTISCERSLRSLWTAHWALPEMDSRIPYDDYPVVFLPAYENP PAWIPPHERVHHPDYNNELTQFLPRTITLKKPPGAQLGFNIRG GKASQLGIFISKVIPDSDAHRAGLQEGDQVLAVNDVDFQDIEH SKAVEILKTAREISMRVRFFPYNYHRQKERTVH
421	1160	3	890	HEQVSALHRRIKAIVEVAAMCGVNIICFQEAWTMPFAFCTREK LPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILERDSEHGD VLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYMEGNLGH PVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNPSATIG ALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTSGDGK KAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDLNLC QQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	ļ	sequence	sequence	
422	1161	5214	352	MAKSGGCGAGAGVGGGNGALTWVNNAAKKEESETANKNDSSKK LSVERVYQKKTQLEHILLRPDTYIGSVEPLTQFMWYDEDVGM NCREVTFVPGLYKIFDEILVNAADNKQRDKNMTCIKVSIDPES NIISIWNNGKGIPVVEHKVEKVYVPALIFGQLLTSSNYDDEK KVTGGRNGYGAKLCNIFSTKFTVETACKEYKHSFKQTWMNNMM KTSEAKIKHFDGEDYTCITFQPDLSKFKMEKLDKDIVALMTRR AYDLAGSCRGVKVMFNGKKLPVNGFRSYVDLYVKDKLDETGVA LKVIHELANERWDVCLTLSEKGFQQISFVNSIATTKGGRHVDY VVDQVVGKLIEVVKKKNKAGVSVKPFQVKNHIWVFINCLIENP TFDSQTKENMTLQPKSFGSKCQLSEKFFKAASNCGIVESILNW VKFKAQTQLNKKCSSVKYSKIKGIPKLDDANDAGGKHSLECTL ILTEGDSAKSLAVSGLGVIGRDRYGVFPLRGKILNVREASHKQ IMENAEINNIIKIVGLQYKKSYDDAQSLKTLRYGKIMIMTDQD QDGSHIKGLLINFIHHNWPSLLKHGFLEEFITPIVKASKNKQE LSFYSIPEFDEWKKHIENQKAWKIKYYKGLGTSTAKEAKEYFA DMERHRILFRYAGPEDDAAITLAFSKKKIDDRKEWLTNFMEDR RQRRLHGLPEQFLYGTATKHLTYNDFINKELILFSNSDNERSI PSLVDGFKPGQRKVLFTCFKRNDKREVKVAQLAGSVAEMSAYH HGEQALMMTIVNLAQNFVGSNNINLLQPIGQFGTRLHGGKDAA SPRYIFTMLSTLARLLFPAVDDNLLKFLYDDNQRVEPEWYIPI IPMVLINGABGIGTGWACKLPNYDAREIVNNVRRMLDGLDPHP MLPNYKNFKGTIQELGQNQYAVSGEIFVVDRNTVEITELPVRT WTQVYKEQVLEPMLNGTDKTPALISDYKEYHTDTTVKFVVKMT EEKLAQAEAAGLHKVFKLQTTLTCNSMVLFDHMGCLKKYETVQ DILKEFFDLRLSYYGLRKEWLVGMLGAEFTKLNNQAFFILEKI QGKITI+NRSKKDLIQMLVQRGYESDVKAWKEAQEKAAEDE TQNQHDDSSDSGTPSGPDFNYILNMSLWSLTKEKVEELIKQR DAKGREVNDLKRKSPSDLWKEDLAAFVEELDKVESQEREDVLA GMSGKAIKGKVGKPKVKKLQLEETMPSPYGRRIIPEITAMKAD ASKKLLKKKGDLDTAAVKVEFDEEFSGAPVEGAGEEALTPSV PINKGPKPKREKKEPGTRVRKTPTSSGKPSAKKVKKRNPWSDD ESKSESDLEETEPVVIPRDSLLRRAAAERPKYTFDFSEEDDD ADDDDDDNDLEELKVKASPITNDGEDEFVPSDGLDKDEYTFS PGKSKATPEKSLHDKKSQDFGNLFSFPSYSQKSEDDSAKFDSNE EEDSASVFSPSFGLKQTDKVPSKTVAAKKGKPSSDTVPKPKRA PKQKKVVEAVNSDSDSEFGIPKKTTTPKGKGRGAKKRKASGSE NEGDYNPGRKTSKTTSKKPKKTSFDQDSDVDIFPSDFPTEPPS
				LPRTGRARKEVKYFAESDEEEDDVDFAMFN
423	1162	1	219	KGCLAASFNCIFLYTGELYPTMIR*VEA*WENDSLFLGKDILL CTGQTPELNQVHPSPKAPPNTHHCKAHSSH

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
424	1163	1454	446	ENSFECKDCGKAFSRGYQLSHHQKIHTGEKPYECKECKKAFRW GNQLTQHQKIHTGEKPYECKDCGKAFRWGSSLVIHKRIHTGEK PYECKDCGKAFRRGDELTQHQRFHTGEKDYECKDCGKTFSRVY KLIQHKRIHSGEKPYECKDCGKAFICGSSLIQHKRIHTGEKPY ECQECGKAFTRVNYLTQHQKIHTGEKPHECKECGKAFRWGSSL VKHERIHTGEKPYKCTECGKAFNCGYHLTQHERIHTGETPYKC KECGKAFIYGSSLVKHERIHTGVKPYGCTECGKSFSHGHQLTQ HQKTHSGAKSYECKECGKACNHLNHLREHQRIHNS
425	1164	826	407	HQYLDDLYPLHVMTILLKSHFFTMLKRPVGSSSFASLPFYHQS ILLRKNQMKRKKTQQDLTHINWTLQAVSIQTCIWLQKKPSSYF HQLPNQVL*PENSGPESCLYDLAAVVVHHGSG
426	1165	464	29	XLDPDTLPAVATLLMDVMFYSNGVKDPMATGDDCGHIRFFSFS LIEGYISLVMDVQTQQRFPSNLLFTSASGELWKMVRIGGQPLG FGPVWESGPTGPTSPLILPVTPSSSHRQAASQVTTTKQGQWLC LKRPSARSPDHTACLG*
427	1166	649	901	EAPLTSVCFSLERRFGSSSNTTSFGTLASQNAPTFGSLSQQTS GFGTQSSGFSGFGSGTGGFSFGSNNS*VSPFLSLTLIKSIK
428	1167	3	340	EEPQGSPIWVWLAGSLTSVSCFLPFQRMRIKPHQGQYIGEMSF LQHHKGECRPQKD*ARQENPCGPCSERRKHLLGQDPKTCKCSC KNTDSRCKARPLELNERTCRCDKPRR
429	1168	355	1312	TLWAGPGLCPQSHSSSSVPAPWEPHVERALRTDRNQGQRPLLS ASWAPAPARPLFLTSPVLLPKSRAIPAARDPS*AGIFCLLEMA GGQASVVIIGSAGVLGCRWGSSGKSHSLSPSRKGNLHLLSQEP QTTVVHNATDGIKGSTESCNTTTEDEDLKVRKQEIIKITEQLI EAINNGDFEAYTKICDPGLTSFEPEALGNLVEGMDFHKFYFEN REWVRAADILLPAPLPLCLCLLLTFSSQLPTFPLFDLRAALLL CMLVPLCPDGCRQAPLKALLLSSKCHSFCSCFVAVPVTTIKLT YFLPGAVAYACNPNTLGG
430	1169	439	728	ERAGAGGAAACRAGTRSGATSRTPWPLHRQLSMMLMLAQSNPQ LFALMGTRAGIARELERVEQQSRLEQLSAAELQSRNQGHWADW LQAYRARLGQ
431	1170	3	440	NGTLFIMVMHIKDLVSDYKE*WL*RKPLPW*EALLLRDCFFF* VTENGADPNPYVKTYLLPDNHKTSKRKTKISRKTRNPTFNEML VYSGYSKETLRQRELQLSVLSAESLRENFFLGGVTLPLKDFNL SKETVKWYQLTAATYL

ID   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.   No.	ara	CEO	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
No. of of	SEQ	SEQ			Amino acid segment containing signal peptide (A=Alamine,
No.					C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
On Mouleic Acids         Amino Acids         Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence         Experiment, V = Valine, W = Tryptophan, Y = Tyrosine, X = Unknown, *=Stop Codon, /=possible nucleotide deletion, acid residue of amino acid sequence           432         1171         433         1824         LHRIMQLAVVUSQULENGSSVLVCLEEGWDITAQVTSLVQLLS DFFYRTLEGFQNLVSKEPLSFGHKFSQRSSLTILNCQGSGPAPV PLOFILL DEDVERLENGTLEFDLYSKEPLSFGHKFSQRSSLTILNCQGSGPAPV PLOFILL DEDVERLENGTLEFDLYSKEPLLAFHYVSINFKYFLL DSDYERLENGTLEFDLYSKEFDNLYSKEPLAFHYVSINFKYFLL DSDYERLENGTLEFDLYSKEPSLAFFNLYSKYSTLHAFHYVSINFKYFLL DSDYERLENGTLYSQVSSLLHALPDSSMGEGENGSISSPNSVARA ATLYSQYTSKNDENRSFEGTLYKRGALLKGWKPRWFVLDVTKH QLRYYDSGEDTSCKGHIDLAEVERWTVDLKEPERTDRSQRHLSS SPEILSTRUSYGVSKSLHALPDSSMGEGENSSISSPNSVARA ATLYSQYTSKNDENRSFEGTLYKRGALLKGWKPRWFVLDVTKH QLRYYDSGEDTSCKGHIDLAEVERWTPAGPSNGARKHTSNKAF FULKTSKRYVNTCADGGGSAQQWMMEKQSGISDA FULKTSKRYVNTCADGGGSAQQWMEKQSGSSGSTARSKAFARTSKAF HRRQSCSVARVGLGLILLLMGAGLAVQGWFLIQLHWRLGEMYT RLPPGBAGSWEQLIQERSHEVWRAAHLIGABASLTGSGGPLL WETQLGLAFTHGLISKTRTRYPEBLELLUSQGSFCGRATSSSRWWD SSPIGGVWLLEAGERVVVRLDERLWRLRGGTSFFGAFMV SSPIGGVWLLEAGERVVVRLDERLWRLRGGTSFFGAFMV SSPIGGVWLLEAGERVVVRLDERLWRLRGGTSFFGAFMV SSPIGGVWLLEAGERVVVRLDERLWRLRGGTSFFGAFMV SSPIGGVWLLEAGERVVVRLDERLWRLRGGTSFFGFGFFSFFF HVLKPSVRGASSPRCGSSFPLAGLIVTSFTTALEC AKMQNAEAADATLVFTGVVVDLABALLVLLGRVRRREDFFD GPYCCRSLDAQLVPQSIMAAATLRTTQVSAASSRPHTSSFT HVLKPSVRGASSPRTHTSFFT HVLKPSVRGASSPRTHTSFFT TWASVNTTHVCGFWGGALLTSFSSLLFYICSRVSTRALEC AKMQNAEAADATLVFTGYVVPALATLYALVLLSRVRRREDFFL AKMQNAEAADATLVFTGYVVPALATLYALVLLSRVRRREDFFL AKMQNAEAADATLVFTGYVVPALATLYALVLLSRVRRREDFFL AKMQNAEAADATLVFTGYVVPALATLYALVLLSRVRRREDFFL AKMQNAEAADATLVFTGSVVFTALLEC AKMQNAEAADATLVFTGSVVFTALLEC AKMQNAEAADATLVFTGYVVPALATLYALVLSRVRRREDFFL AKMQNAEAATLYAPSVNTTHVCVCVCIYL SVVVSKSSAEADCVLQPRRHPASILLVFATSISESSLLIFSFQ KYEEKLIVFAVSLAAK PFEREGRERFFTMYSTA					F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
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Action of first amino acid residue of amino acid sequence of amino acid sequence of amino acid sequence sequence   LHRIMQLAVVSQVLENGSSVLVCLEEGWDITAQVTSLVQLLS DPYTRTLEGFQMLVEKEMLSFGHKFSQRSSLTINCQGSGFAPW		1	-		P=Proline, O=Glutamine, R=Arginine, S=Serine,
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1174 27 1139 LWWPPLSRHAAHRQWPGPTAPRGLGHKVKGRGASPAAMWSCSW FNGTGLVEELPACQDLQLGLSLLSLLGLVVGVPVGLCYNALLV LANLHSKASMTMPDVYFVNMAVAGLVLSALAPVHLLGPPSSRW ALWSVGGEVHVALQIPFNVSSLVAMYSTALLSLDHYIERALPR TYMASVYNTRHVCGFVWGGALLTSFSSLLFYICSHVSTRALEC AKMQNAEAADATLVFIGYVVPALATLYALVLLSRVRREDTPLD RDTGRLEPSAHRLLVATVCTQFGLWTPHYLILLGHTVIISRGK PVDAHYLGLLHFVKDFSKLLAFSSSFVTPLLYRYMNQSFPSKL QRLMKKLPCGDRHCSPDHMGVQQVLA  436 1175 322 756 SESELFTLMPSLPTTNCVHSLQMIPPLSPAPNQELVLGLCYMS YLAFLYMTFDFCCLYFSTVYAPSFKYICVHTDTHICVCVCIYL SSVVSKSSAEADGVLQPRRHPASLLIVFATSISESSLLIFSFQ KTEAKLIVFAVSLAAK  437 1176 2 153 FFFLRQSLTLSPRLECSGATSASPSAGITGMSHHSQPIVNFLR ACIPISK  438 1177 1 692 RQHAEERGRRNPKTGLTLERVGPESSPYLLRRHQRQGQEGEHY HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG		ļ			GPYQCRPSLPAQLYPQSLMAAATLRTPTQVSAASSRPHTPSPT
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PVDAHYLGLLHFVKDFSKLLAFSSSFVTPLLYRYMNQSFPSKL QRLMKKLPCGDRHCSPDHMGVQQVLA  436 1175 322 756 SESELFTLMPSLPTTNCVHSLQMIPPLSPAPNQELVLGLCYMS YLAFLYMTFDFCCLYFSTVYAPSFKYICVHTDTHICVCVCIYL SSVVSKSSAEADGVLQPRRHPASLLIVFATSISESSLLIFSFQ KTEAKLIVFAVSLAAK  437 1176 2 153 FFFLRQSLTLSPRLECSGATSASPSAGITGMSHHSQPIVNFLR ACIPISK  438 1177 1 692 RQHAEERGRRNPKTGLTLERVGPESSPYLLRRHQRQGQEGEHY HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG			l	1	·
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YLAFLYMTFDFCCLYFSTVYAPSFKYICVHTDTHICVCVCIYL SSVVSKSSAEADGVLQPRRHPASLLIVFATSISESSLLIFSFQ KTEAKLIVFAVSLAAK  437 1176 2 153 FFFLRQSLTLSPRLECSGATSASPSAGITGMSHHSQPIVNFLR ACIPISK 438 1177 1 692 RQHAEERGRRNPKTGLTLERVGPESSPYLLRRHQRQGQEGEHY HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG	125	1175	1322	756	
SSVVSKSSAEADGVLQPRRHPASLLIVFATSISESSLLIFSFQ KTEAKLIVFAVSLAAK  437 1176 2 153 FFFLRQSLTLSPRLECSGATSASPSAGITGMSHHSQPIVNFLR ACIPISK  438 1177 1 692 RQHAEERGRRNPKTGLTLERVGPESSPYLLRRHQRQGQEGEHY HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG	430	11/3	222	1,50	
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ACIPISK  438 1177 1 692 RQHAEERGRRNPKTGLTLERVGPESSPYLLRRHQRQGQEGEHY HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG	45=	1	ļ	1153	
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HSCVQLAPTRGLEES/GHGPL/SLAGGPRVGGV/AAAATEAPR MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG		1	<u> </u>	<del> </del>	
MEWKVKVRSDGTRYVAKRPVRDRLLKARALKIREERSGMTTDD DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG	438	1177	1	692	
DAVSEMKMGRYWSKEERKQHLIRAREQRKRREFMMQSRLECLR EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG					i i
EQQNGDSKPELNIIALSHRKTMKKRNKKILDNWITIQEMLAHG	J		]		)
		1			
1 I STANDAYDER TO THE TOTAL	1				1 - 2
ARSADGKRVYNPLLSVTTV				<u> </u>	ARSADGKRVYNPLLSVTTV

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	согте-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
1	1	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
ļ		acid	acid	\=possible nucleotide insertion)
		residue	residue	(-possible indefedited insertion)
ĺ	ļ	of amino	of amino	
		acid	acid	
	1	sequence	sequence	
439	1178	2	616	SDRGCSAAAGRNMTAVGVQAQRPLGQRQPRRSFFESFIRTLII
		_	1	TCVALAVVLSSVSICDGHWLLAEDRLFGLWHFCTTTNQSVPIC
			ļ	FRDLGQAHVPGLAVGMGLVRSVGALAVVAAIFGLEFLMVSQLC
		1	1	EDKHSQCKWVMGSILLLVSFVLSSGGLLGFVILLRNQVTLIGF
ļ	ĺ			TLMFWCEFTASFLLFLNAISGLHINSITHPWE
440	1179	2	540	QILPNLYLGSARDSANLESLAKLGIRYILNVTPNLPNFFEKNG
110	/-	] _	1	DFHYKQIPISDHWSQNLSRFFPEAIEFIDEALSQNCGVLVHCL
	1			AGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFM
į.	1			GQLLDFERSLRLEERHSQEQGSGGQASAASNPPSFFTTPTSDG
]	}	j		AFELAPT
441	1180	940	463	RKSLHENKLKRLQEKVEVLEAKKEELETENQVLNRQNVPFEDY
441	1100	1 220	100	TRLQKRLKDIQRRHNEFRSLILVPNMPPTASINPVSFQSSAMG
		İ		SKHGTTISSSYAGGTTSKGTLSTSQKTRRTGNNTKKTTRGTWI
				FRRMMFLENRQIKRGEVGDSVKLDILTCGI
442	1181	1	986	GRPGAGASELFPSVTTDLSVSKQNACLTCVDFVTVHVCMGFWG
444	1101	1 -	300	IGPGALSTSCIPYPLSHGPGSVKAEMLHMYSQKDPLILCVRLA
ļ	1	]	1	VLLAVTLTVPVVLFPIRRALQQLLFPGKAFSWPRHVAIALILL
				VLVNVLVICVPTIRDIFGVIGSTSAPSLIFILPSIFYLRIVPS
1				EVEPFLSWPKIQALCFGVLGVLFMAVSLGFMFANWATGQSRMS
			Į	GH*SGPAGPGPCAHAHGGVRAAP*GPSCPTCGGGWFP*TWLSE
			1	AGDSRGCRLAHFPPPQGCQAWIMALIPTPTPWEEEEEEEEE
				EEEEEEEARSWWSLCPAQSSLPPPG
443	1182	460	27	INELRYHLEESRDKNVLLCLEERDWDPGLAIIDNLMQSINQSK
443	1102	1 400	2'	KTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIIFILLEPV
				LQHSQYLRLRQRICKSSILQWPDNPKAEGLFWQTLRNVVLTEN
				DSRYNNMYVDSIKQY
444	1183	1682	230	DDPIKTSWTPPRYVLSMSEERHERVRKKYHILVEGDGIPPPIK
444	1,103	1002	230	SFKEMKFPAAILRGLKKKGIHHPTPIQIQGIPTILSGRDMIGI
		1		AFTGSGKTLVFTLPVIMFCLEQEKRLPFSKREGPYGLIICPSR
1	1	1.		ELAROTHGILEYYCRLLQEDSSPLLRCALCIGGMSVKEQMETI
-	1			RHGVHMMVATPGRLMDLLQKKMVSLDICRYLALDEADRMIDMG
1	1			FEGDIRTIFSYFKGQRQTLLFSATMPKKIQNFAKSALVKPVTI
ļ	1			NVGRAGAASLDVIQEVEYVKEEAKMVYLLECLQKTPPPVLIFA
		1		EKKADVDAIHEYLLLKGVEAVAIHGGKDQEERTKAIEAFREGK
				KDVLVATDVASKGLDFPAIQHVINYDMPEEIENYVHRIGRTGR
			1	SGNTGIATTFINKACDESVLMDLKALLLEAKQKVPPVLQVLHC
				GDESMLDIGGERGCAFCGGLGHRITDCPKLEAMQTKQVSNIGR
				KDYLAHSSMDF
1	1104	<del>                                     </del>	375	IETTQPSEDTNANSQDNSMQPETSSQQQLLSPTLSDRGGSRQD
445	1184	1 -	3/3	AADAGKPQRKFGQWRLPSAPKPISHSVSSVNLRFGGRTTMKSV
1		1		VCKMNPMTDAASCGSEVKKWWTRQLTVESDESGDDLLDI
1	1,,,,	12	223	NDRFSACYFTLKLKEAAVRQREALKKLTKNIATDSYISVNLRD
446	1185	1 2	223	VYARSIMEMLRLKGRERASTRSSGGDDFWF
				A LUCY THE LITTING WINDS THOUGH IN

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of		corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-		P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		to first	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		amino	acid	
		acid residue	residue	\=possible nucleotide insertion)
		of amino	of amino	
1		acid	acid	
		sequence	sequence	·
447	1186	2	1031	FTVFILGITIRPLVEFLDVKRSNKKQQAVSEEIYCRLFDHVKT
44/	1100	-	1031	GIEDVCGHWGHNFWRDKFKKFDDKYLRKLLIRENQPKSSIVSL
			1	YKKLEIKHAIEMAETGMISTVPTFASLNDCREEKIRKVTSSET
				DEIRELLSRNLYQIRQRTLSYNRHSLTADTSERQAKEILIRRR
ļ		l .		HSLRESIRKDSSLNREHRASTSTSRYLSLPKNTKLPEKLQKRR
				TISIADGNSSDSDADAGTTVLNLQPRARRFLPEQFSKKSPQSY
1				
	1	l		KMEWKNEVDVDSGRDMPSTPPTPHSREKGTQTSGLLQQPLLSK
			<u> </u>	DQSGSEREDSLTEGIPPKPPPRLVWRASEPGSRKARFGSEKP
448	1187	3	444	HEEASGLSVWMGKQMEPLHAVPPAAITLILSLLVAVFTECTSN
		ļ	1	VATTTLFLPIFASMSRSIGLNPLYIMLPCTLSASFAFMLPVAT
1		1		PPNAIVFTYGHLKVADMVKTGVIMNIIGVFCVFLAVNTWGRAI
			j	FDLDHFPDWANVTHIET
449	1188	3	125	HELENNWLQHEKAPTEEGKKELLALSNANPSLLERHCAYL
450	1189	1	188	GNIIYMYMQPGARSSQDQGKFLTLFYNIVTPLLNPLIYTLRNR
1		1		EVKGALGRLLLGKRELGKE
451	1190	1.0	1879	PLEQRSNCRVDPRVRTHTMASDTSSLVQSHTYKKREPADVPYQ
.	1	1		TGQLHPAIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPW
	1		1	DSAKKDENRMKNRYGNIIAYDHSRVRLQTIEGDTNSDYINGNY
	1	1		IDGYHRPNHYIATQGPMQETIYDFWRMVWHENTASIIMVTNLV
1		Ì		EVGRVKCCKYWPDDTEIYKDIKVTLIETELLAEYVIRTFAVEK
		ı		RGVHEIREIRQFHFTGWPDHGVPYHATGLLGFVRQVKSKSPPS
	1		1	AGPLVVHCSAGAGRTGCFIVIDIMLDMAEREGVVDIYNCVREL
1	}	l .		RSRRVNMVQTEEQYVFIHDAILEACLCGDTSVPASQVRSLYYD
	1		1	MNKLDPQTNSSQIKEEFRTLNMVTPTLRVEDCSIALLPRNHEK
			1	NRCMDILPPDRCLPFLITIDGESSNYINAALMDSYKQPSAFIV
		Ì		TQHPLPNTVKDFWRLVLDYHCTSVVMLNDVDPAQLCPQYWPEN
1	i			GVHRHGPIQVEFVSADLEEDIISRIFRIYNAARPQDGYRMVQQ
	1		1	FOFLGWPMYRDTPVSKRSFLKLIRQVDKWQEEYNGGEGRTVVH
	ĺ			CLNGGGRSGTFCAISIVCEMLRHQRTVDVFHAVKTLRNNKPNM
1		1	ļ	VDLLDQYKFCYEVALEYLNSG
452	1191	603	342	PLTYNKKYTYPWWGDALGWLLALSSMVCIPAWSLYRLGTLKGP
452	11791	1 803	342	FRERIRQLMCPAEDLPQRNPAGPSAPATPRTSLLRLTELESHC
453	1100	120	449	TLSESGALFSLGPPPLSLKSSSAPRPYSTLRDCLEHFAELFDL
453	1192	120	"""	GFPNPLAERIIFETHQIHFANCSLGQPTFSDPPEDVLLAMIIA
				PICLIPFLITLVVWRSKDSEAQA
454	11702	1838	1066	CEEREQEKDDVDVALLPTIVEKVILPKLTVIAENMWDPFSTTQ
454	1193	1030	1000	TSRMVGITLKLINGYPSVVNAENKNTQVYLKALLLRMRRTLDD
1	1		1	DVFMPLYPKNVLENKNSGPYLFFQRQFWSSVKLLGNFLQWYGI
		1		FSNKTLQELSIDGLLNRYILMAFQNSEYGDDSIKKAQNVINCF
				PKQWFMNLKGERTISQLENFCRYLVHLADTIYRNSIGCSDVEK
	1			RNARENIKQIVKLLASVRALDHAMSVASDHNVKEFKSLIEGK
L			<u> </u>	NUMBER 17/21 ATTENDED AND CHILD A LOTTED AND CHILD A LOTTED AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CHILD AND CH

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	'	acid	acid	\=possible nucleotide insertion)
	]	residue	residue	possion incomes incomes,
		of amino	of amino	
		acid	acid	,
	1	sequence	sequence	
455	1194	112	1361	TPFCFLCSLVFRSRVWAEPCLIDAAKEEYNGVIEEFLATGEKL
				FGPYVWGRYDLLFMPPSFPFGGMENPCLTFVTPCLLAGDRSLA
	'	Ì		DVIIHEISHSWFGNLVTNANWGEFWLNEGFTMYAQRRISTILF
		ļ	l	GAAYTCLEAATGRALLRQHMDITGEENPLNKLRVKIEPGVDPD
			Į.	DTYNETPYEKGFCFVSYLAHLVGDQDQFDSFLKAYVHEFKFRS
ļ	ŀ			ILADDFLDFYLEYFPELKKKRVDIIPGFEFDRWLNTPGWPPYL
l	1	]	1	PDLSPGDSLMKPAEELAQLWAAEELDMKAIEAVAISPWKTYQL
		ì	ļ	VYFLDKILQKSPLPPGNVKKLGDTYPSISNARNAELRLRWGQI
	1	l	1	VLKNDHQEDFWKVKEFLHNQGKQKYTLPLYHAMMGGSEVAQTL
1	<u> </u>		ł	AKETFASTASQLHSNVVNYVQQIVAPKGS
456	1195	1	889	CASGSSGWRPVLWAGAFTMASAELDYTIEIPDQPCWSQKNSPS
4.56	1175	*	005	PGGKEAETRQPVVILLGWGGCKDKNLAKYSAIYHKRGCIVIRY
1		ļ		TAPWHMVFFSESLGIPSLRVLAQKLLELLFDYEIEKEPLLFHV
	} .		ļ	FSNGGVMLYRYVLELLQTRRFCRLRVVGTIFDSAPGDSNLVGA
		Í	1	LRALAAILERRAAMLRLLLLVAFALVVVLFHVLLAPITALFHT
			1	HFYDRLQDAGSRWPELYLYSRADEVVLARDIERMVEARLARRV
ļ				LARSVDFVSSAHVSHLRDYPTYYTSLCVDFMR\NWVRC
L	1305		295	PRVRDRLPSTGVRDRKGDKPWKESGGSVEAPRMGFTHPPGHLS
457	1196	2	295	GCOSSLASGETGTGSADPPGGPRPGLTRRAPVKDTPGRAPAAD
İ		1		AAPAGPSSCLG
		<u> </u>	1	QGRTSCIGLYTYQRRICKYRDQYNWFFLARPTTFAIIENLKYF
458	1197	1299	682	LLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSL
İ		1	1	LNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGK
			Į.	DVFNTKSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQM
}	İ			
				HVMMYGVYRLRAFG\HIFNDALVFLPPNGSDND
459	1198	779	61	HEGKPTRGRGRGGSLSTRGRGSEVPDSAHLAPTPLFSESGCCG
	1			LRSRFLTDCKMEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVS
		i		GFLLFRSLPRHTFGLVQSKLFPFYFHISMGCAFINLCILASQH
	1			AWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQT
j			]	VEKERGLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHG
1		ļ	<u> </u>	LSSLCNLGCVLSNGLCLA\ALPWK
460	1199	517	815	KQLDKQLRADPSGSLPPLPPSPPPPLEAGGRPPEVP/PRGPSA
	1		1	VPSFPSVSGDWGGPVEAG/EGGQQGRGRARARPCSLPPLLPPS
1			1	PVCRLSGSRAPLGCDG
461	1200	1	583	RNQLSSQKSVPWVPILKSLPLWAIVVAHFSYNWTFYTLLTLLP
	1		1	TYMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRAKW
1	1			NFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLTIS
1	1			TTLGGFCSSGFSINHLDIAPSYAGILLGITNTFATIPGMVGPV
1			1	IAKSLTPDMGISLHRPGWSAVA -
462	1201	25	383	GPSGTTHASAHSGHPGSPRGSLSRHPSSQLAGPGVEGGEGTQK
102		1		PRDYIILAILSCFCPMWPVNIVAFAYAVMSRNSLQQGDVDGAQ
1				RLGRVAKLLSIVALVGGVLIIIASCVINLGVYK
463	1202	573	372	SLFLSFPPLSFKMTLNDAMRNKARLSITGSTGENGRVMTPEFP
-203	1202	7,3	1 - 7 -	KAVHAVPYVSPGMGMNVSVTDLS
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to first amino acid residue of amino acid sequence sequence  464 1203 2018 491 DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVAD VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	GGV EVA GSW HTS EDL GGG WME QFE
acid residue of amino acid sequence sequence  464 1203 2018 491 DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVAD VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	GGV EVA GSW HTS EDL GGG WME QFE
residue of amino acid sequence sequence sequence sequence vDDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVAD vDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	EVA GSW HTS EDL GGG WME QFE
of amino acid sequence sequence  464 1203 2018 491 DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVAD VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	EVA GSW HTS EDL GGG WME QFE
acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequenc	EVA GSW HTS EDL GGG WME QFE
sequence sequence  464 1203 2018 491 DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVAD  VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL  GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT  RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA  DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL  DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE  TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG  DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK  RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL  EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	EVA GSW HTS EDL GGG WME QFE
464 1203 2018 491 DDVPPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPPEVAD VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	EVA GSW HTS EDL GGG WME QFE
VDSGVYAVPPPAEREAPAEGKRLSASSTGSTRSSQSASSL GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	EVA GSW HTS EDL GGG WME QFE
GPGREPLELEVAVEALARLQQGVSATVAHLLDLAGSAGAT RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEFFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	GSW HTS EDL GGG WME QFE
RSPSEPQEPLVQDLQAAVAAVQSAVHELLEFARSAVGNAA DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	HTS EDL GGG WME QFE
DRALHAKLSRQLQKMEDVHQTLVAHGQALDAGRGGSGATL DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	EDL GGG WME QFE
DRLVACSRAVPEDAKQLASFLHGNASLLFRRTKATAPGPE TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	GGG WME QFE
TLHPNPTDKTSSIQSRPLPSPPKFTSQDSPDGQYENSEGG DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	wme Qfe
DYDYVHLQGKEEFEKTQKELLEKGSITRQGKSQLELQQLK RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	QFE
RLEQEVSRPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLL EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	
EQCEANLTTLTNAVDAFFTAVATNQPPKIFVAHSKFVILS	FYL
LVFIGDTLSROAKAADVRSOVTHYSNLLCDLLRGIVATTK	
	AAA
LQYPSPSAAQDMVERVKELGHSTQQFRRVLGQLAAA	
465 1204 299 189 EMEEPQKSYVNTMDLERDEPLKSTGPQISVSEFSCHCCYD	ILV
NPTTLNCGHSFCRHCLALWWASSKKTECPECREKWEGFPK	VSI
LLRDAIEKLFPDAIRLRFEDIQQNNDIVQSLAAFQKYGND	QIP
LAPNTGRANQQMGGGFFSGVLTALTGVAVVLLVYHWSSRE	SEH
DLLVHKAVAKWTAEEVVLWLEQLGPWASLYRERFLSERVN	GRL
LLTLTEEEFSKTPYTIENSSHRRAILMELERVKALGVKPF	QNL
WEYKAVNPGRSLFLLYALKSSPRLSLLYLYLFDYTDTFLF	FIH
TICPLQEDSSGEDIVTKLLDLKEPTWKQWREFLVKYSFLF	YQL
IAEFAWDWLEVHYWTSRFLIINAMLLSVLELFSFWRIWSR	SEL
K*VGFRFLRLGVAALGSVEVAGLRGVVKGERPLLYGHGAG	ARF
PHSVLLLPVAKPLPLPLLPRGLC	
466 1205 2 242 EKARMIYEDYISILSPKEVSLDSRVREVINRNLLDPNPHM	YED
AQLQIYTLMHRDSFPRFLNSQIYKSFVESTAGSSSES	
467 1206 2 619 LYYSQDEESKIMISDFGLSKMEGKGDVMSTACGTPGYVAE	EVL
AQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDSKLFEQI	
EYEFDSPYWDDISDSAKDFIRNLMEKDPNKRYTCEQAAR	
AGDTALNKNIHESVSAQIRKNFAKSKWRQAFNATAVVRHM	
HLGSSLDSSNASVSSSLSLASQKDCASGTFHAL	
468 1207 1 352 RTRGGAVSFEDFIKGLSILLRGTVQEKLNWAFNLYDINKL	GYI
TKEEMLDIMKAIYDMMGKCTYPVLKEDAPRQHVETFFQKM	
KDGVVTIDEFIESCQKDENIMRSMQLFENVI	
469 1208 3 1015 PRSPEHHTPAWHEGRSLGPIMASMADRNMKLFSGRVVPAC	GEE
TFENWLTQVNGVLPDWNMSEEEKLKRLMKTLRGPAREVME	
ATNPNLSVADFLRAMKLVFGESESSVTAHGKFFNTLQAQO	
SLYVIRLEVQLQNAIQAGIIAEKDANRTRLQQLLLGGELS	
RLRLKDFLRMYANEQERLPNFLELIKMVREEEDWDDAFII	
	77.77
PKRSESMVERAVSPVAFQGSPPIVIGSADCNVIEIDDTLI	
EDVILVESQDPPLPSWGAPPLRDRARPQDEVLVIDSPHNS	DSD
FPSTSGGSGYKNNGPGEMRRARKRKHTIRCSYCGEE	DSD
470 1209 1543 1351 SVACTVPLRSMSDPDQDFDKEPDSDSTKHSTPSNSSNPSO	DSD RAQ
PNSPHRSQLPLEGLEQPACDT	DSD RAQ

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, _possible nucleotide insertion)
471	1210	3	952	YSAVEFAERGSGSSGDELREDDEPVKKRGRKGRGREPPSSSD SEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRVRPEEKQQ AKPVKVERTRKRSEGFSMDRKVEKKKEPSVÈEKLQKLHSEIKF ALKVDSPDVKRCLNALEELGTLQVTSQILQKNTDVVATLKKIR RYKANKDVMEKAAEVYTRLKSRVLGPKIEAVQKVNKAGMEKEK AEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGES AEDKEHEEGRDSEEGPRCGSSEDLHDSVREGPDLDRPGSDRQE RERARGDSEALDEES
472	1211	5204	2901	LAELSSLSVLRLSHNSISHIAEGAFKGLRSLRVLDLDHNEISG TIEDTSGAFSGLDSLSKLTLFGNKIKSVAKRAFSGLEGLEHLN LGGNAIRSVQFDAFVKMKNLKELHISSDSFLCDCQLKWLPPWL IGRMLQAFVTATCAHPESLKGQSIFSVPPESFVCDDFLKPQII TQPETTMAMVGKDIRFTCSAASSSSSPMTFAWKKDNEVLTNAD MENFVHVHAQDGEVMEYTTILHLRQVTFGHEGRYQCVITNHFG STYSHKARLTVNVLPSFTKTPHDITIRTTTMARLECAATGHPN PQIAWQKDGGTDFPAARERRMHVMPDDDVFFITDVKIDDAGVY SCTAQNSAGSISANATLTVLETPSLVVPLEDRVVSVGETVALQ CKATGNPPPRITWFKGDRPLSLTERHHLTPDNQLLVVQNVVAE DAGRYTCEMSNTLGTERAHSQLSVLPAAGCRKDGTTVGIFTIA VVSSIVLTSLVWVCIIYQTRKKSEEYSVTNTDETVVPPDVPSY LSSQGTLSDRQETVVRTEGGPQANGHIESNGVCPRDASHFPEP DTHSVACRQPKLCAGSAYHKKPWKAMEKAEGTPGPHKMEHGGR VVCSDCNTEVDCYSRGQAFHPQPVSRDSAQPSAPNGPEPGGSD QEHSPHHQCSRTAAGSCPECQGSLYPSNHDRMLTAVKKKPMAS LDGKGDSSWTLARLYHPDSTELQPASSLTSGSPERAEAQYLLV SNGHLPKACDASPESTPLTGQLPGKQRVPLLLAPKS



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
473	1212	2	2466	AAAGAARRVSVRCGRSGPGPGRGAAGLSPADIALASEQGASCS VRAPERKLRMKLLWQAKMSSIQDWGEEVEEGAVYHVTLKRVQI QQAANKGARWLGVEGDQLPPGHTVSQYETCKIRTIKAGTLEKL VENLLTAFGDNDFTYISIFLSTYRGFASTKEVLELLLDRYGNL TSPNCEEDGSQSSSESKMVIRNAIASILRAWLDQCAEDFREPP HFPCLQKLLDYLTRMMPGSDPERRAQNLLEQFQKQEVETDNGL PNTISFSLEEEEELEGGESAEFTCFSEDLVAEQLTYMDAQLFK KVVPHHCLGCIWSRRDKKENKHLAPTIRATISQFNTLTKCVVS TILGGKELKTQQRAKIIEKWINIAHECRLLKNFSSLRAIVSAL QSNSIYRLKKTWAAVPRDRMLMFEELSDIFSDHNNHLTSRELL MKEGTSKFANLDSSVKENQKRTQRRLQLQKDMGVMQGTVPYLG TFLTDLTMLDTALQDYIEGGLINFEKRREFEVIAQIKLLQSA CNSYCMTPDQKFIQWFQRQQLLTEEESYALSCEIEAAADASTT SPKPWKSMVKRLNLLFLGADMITSPTPTKEQPKSTASGSSGES MDSVSVSSCESNHSEAEEGYITPMDTPDEPQKKLSESSSYCSS IHSMDTNFLQGMSSLINPLSSPPSCNNNPKIHKRSVSVTSITS TVLPPVYNQQNEDTCIIRISVEDNNGNMYKSIMLTSQDKTPAV IQRAMLKHNLDSDPAEEYELVQVISEDKELVIPDSANVFYAMN SQVNFDFILRKKNSMEEQVKLRSRTSLTLPRTAKRGCWSNRHS
474	1213	1	867	AREKMDSCIEAFGTTKQKRALNTRRMNRVGNESLNRAVAKAAE TIIDTKGVTALVSDAIHNDLQDDSLYLPPCYDDAAKPEDVYKF EDLLSPAEYEALQSPSEAFRNVTSEEILKMIEENSHCTFVIEA LKSLPSDVESRDRQARCIWFLDTLIKFRAHRVVKRKSALGPGV PHIINTKLLKHFTCLTYNNGRLRNLISDSMKAKITAYVIILAL HIHDFQIDLTVLQRDLKLSEKRMMEIAKAMRLKISKRRVSVAA GSEEDHKLGTLSLPLPPAQTSDRLAKRRKIT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
475	1214		2621	LSLFGSRALGRSGARAMAKAKKVGARRKASGAPAGARGGPAKA NSNPFEVKVNRQKFQILGRKTRHDVGLPGVSRARALRKRTQTL LKEYKERDKSNVFRDKRFGEYNSNMSPEEKMMKRFALEQQRHH EKKSIYNLNEDEELTHYGQSLADIEKHNDIVDSDSDAEDRGTL SGELTAAHFGGGGGLLHKKTQQEGEEREKPKSRKELIEELIAK SKQEKRERQAQREDALELTEKLDQDWKEIQTLLSHKTPKSENR DKKEKPKPDAYDMMVRELGFEMKAQPSNRMKTEAELAKEEQEH LRKLEAERLRRMLGKDEDENVKKPKHMSADDLNDGFVLDKDDR RLLSYKDGKMNVEEDVQEEQSKEASDPESNEEEGDSSGGEDTE ESDSPDSHLDLESNVESEEENEKPAKEQRQTPGKGLISGKERA GKATRDELPYTFAAPESYEELRSLLLGRSMEEQLLVVERIQKC NHPSLAEGNKAKLEKLFGFLLEYVGDLATDDPPDLTVIDKLVV HLYHLCQMFPESASDAIKFVLRDAMHEMEEMIETKGRAALPGL DVLIYLKITGLLFPTSDFWHPVVTPALVCLSQLLTKCPILSLQ DVVKGLFVCCLFLEYVALSQRFIPELINFLLGILYIATPNKAS QGSTLVHPFRALGKNSELLVVSAREDVATWQQSSLSLRWASRL RAPTSTEANHIRLSCLAVGLALLKRCVLMYGSLPSFHAIMGPL RALLTDHLADCSHPQELQELCQSTLTEMESQKQLCRPLTCEKS KPVPLKLFTPRLVKVLEFGRKQGSSKEEQERKRLIHKHKREFK GAVREIRKDNQFLARMQLSEIMERDAERKRKVKQLFNSLATQE GEWKALKRKKFKK
476	1215	3	961	LTKQEDCCGSIGTAWGQSKCHKCPQLQYTGVQKPGPVRGEVGA DCPQGYKRLNSTHCQDINECAMPGVCRHGDCLNNPGSYRCVCP PGHSLGPSRTQCIADKPEEKSLCFRLVSPEHQCQHPLTTRLTR QLCCCSVGKAWGARCQRCPTDGTAAFKEICPAGKGYHILTSHQ TLTIQGESDFSLFLHPDGPPKPQQLPESPSQAPPPEDTEEERG VTTDSPVSEERSVQQSHPTATTTPARPYPELISRPSPPTMRWF LPDLPPSRSAVEIAPTQVTETDECRLNQNICGHGECVPGPPDY SCHCNPGYRSHPQHRYCV

CEO	033	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	beginning	end	Amino acid segment containing signal peptide (A—Atamine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	согте-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic Acids	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acias	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	(—possible indicorde insertion)
		of amino	of amino	
		acid	acid	
		sequence	sequence	
477	1216	3652	1207	MAGGHCGSFPAAAAGSGEIVQLNVGGTRFSTSRQTLMWIPDSF
<b>4</b> ,,		3032		FSSLLSGRISTLRDETGAIFIDRDPAAFAPILNFLRTKELDLR
	l		İ	GVSINVLRHEAEFYGITPLVRRLLLCEELERSSCGSVLFHGYL
	ŀ	}		PPPGIPSRKINNTVRSADSRNGLNSTEGEARGNGTQPVLSGTG
			1	EETVRLGFPVDPRKVLIVAGHHNWIVAAYAHFAVWYRIKESSG
	j	}	}	WQQVFTSPYLDWTIERVALNAKVVGGPHGDKDKMVAVASESSI
			ĺ	ILWSVQDGGSGSEIGVFSLGVPVDALFFIGNQLVATSHTGKVG
	[			VWNAVTQHWQVQDVVPITSYDTAGSFLLLGCNNGSIYYIDMQK
	ì			
		1	ļ	FPLRMKDNDLLVTELYHDPSNDAITALSVYLTPKTSVSGNWIE
				IAYGTSSGAVRVIVQHPETVGSGPQLFQTFTVHRSPVTKIMLS
1				EKHLVSVCADNNHVRTWTVTRFRGMISTQPGSTPLASFKILSL
			1	EETESHGSYSSGNDIGPFGERDDQQVFIQKVVPITNKLFVRLS
	ł	ļ		STGKRICEIQAVDCTTISSFTGRECEGSSRMGSRPRRYLFTGH
		1	1	TNGSIQMWDLTTAMDMVNKSEDKDVGGPTEEELLKLLDQCDLS
		ł		TSRCATPNISPATSVVQHSHLRESNSSLQLQHHDTTHEAATYG
	1	1		SMRPYRESPLLARARRTESFHSYRDFQTINLNRNVERAVPENG
	1	l	1	NLGPIQAEVKGATGECNISERKSPGVEIKSLRELDSGLEVHKI
	ļ	1		AEGFSESKKRSSEDENENKIEFRKKGGFEGGGFLGRKKVPYLA
}		İ	1	SSPSTSDGGTDSPGTASPSPTKTTPSPRHKKSDSSGQEYSL
478	1217	1	1379	RRPTRPILTDELFKRTIQLPHLKTLILNGNKLETLSLVSCFAN
1770		\		NTPLEHLDLSQNLLQHKNDENCSWPETVVNMNLSYNKLSDSVF
	Į	Ĭ	1	RCLPKSIQILDLNNNQIQTVPKETIHLMALRELNIAFNFLTDL
			1	PGCSHFSRLSVLNIEMNFILSPSLDFVQSCQEVKTLNAGRNPF
]			1	RCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLNLRGTRLKDV
	İ	1		HLHELSCNTALLIVTIVVIMLVLGLAVAFCCLHFDLPWYLRML
Ì		1		GQCTQTWHRVRKTTQEQLKRNVRFHAFISYSEHDSLWVKNELI
	-	]	)	PNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSIFVL
1		1		SPNFVQNEWCHYEFYFAHHNLFHENSDHILLILLEPIPFYCIP
		1		TRYHKLKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLAT
	1		i	i
				REMYELQTFTELNEESRGSTISLMRTDCL
479	1218	1	1099	PTRPPTRPPTRPLLTPSWTSTGRMWSHLNRLLFWSIFSSVTCR
				KAVLDCEAMKTNEFPSPCLDSKTKVVMKGQNVSMFCSHKNKSL
				QITYSLFRRKTHLGTQDGKGEPAIFNLSITEAHESGPYKCKAQ
1				VTSCSKYSRDFSFTIVDPVTSPVLNIMVIQTETDRHITLHCLS
	1			VNGSLPINYTFFENHVAISPAISKYDREPAEFNLTKKNPGEEE
				EYRCEAKNRLPNYATYSHPVTMPSTGGDSCPFCLKLLLPGLLL
		1	1	LLVVIILILAFWVLPKYKTRKAMRNNVPRDRGDTAMEVGIYAN
1		1	1	ILEKQAKEESVPEVGSRPCVSTAQDEAKHSQELQYATPVFQEV
	1			APREQEACDSYKSGYVYSELNF
480	1219	1	293	FFFFEERRTGSHSVGHPRMEYSGVSMAHCSLNLLGSSNSPSSA
1 300	1223	1	1	SQDARTTGACQHAQLIGFFFF\VETASPQVTHAG/LKHLVSRN
1	1		1	PSAVTSOSARIKT
			1	I DEL INCOMITAL

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID I	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre- sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	/=possible nucleotide insertion/
		of amino	of amino	
		acid	acid	
		sequence	sequence	
481	1220	1	727	NREGARKIONKWLRPSPRSHRTPESVSPERYSYGTSSSSKRTE
1				GSCRRRQSSSSANSQQGQWETGSPPTKRQRRSRGRPSGGAKR
	İ			RRRGAPAAPQQQSEPARPSSEGKVTCDIRLRVRAEYCEHGPAL
				EOGVASRRPQALARQLDVFGQATAVLRSRDLGSVVCDIKFSEL
				SYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLLVSV
İ		ļ·		DEADYEAGRRRLLLMEEEGGRRPTEAS
482	1221	ī	1321	APNTAELRICRVNKNCGSVRGGDEIFLLCDKVQKDDIEVRFVL
102		ļ ⁻		NDWEAKGIFSQADVHRQVAIVFKTPPYCKAITEPVTVKMQLRR
1		ŀ	İ	PSDQEVSESMDFRYLPDEKDTYGNKAKKQKTTLLFQKLCQDHV
			}	ETGFRHVDODGLELLTSGDPPTLASQSAGITVNFPERPRPGLL
1	1	j	}	GSIGEGRYFKKEPNLFSHDAVVREMPTGVSSQAESYYPSPGPI
	1			SSGLSHHASMAPLPSSSWSSVAHPTPRSGNTNPLSSFSTRTLP
1	1			SNSQGIPPFLRIPVGNDLNASNACIYNNADDIVGMEASSMPSA
		<b>!</b>		DLYGISDPNMLSNCSVNMMTTSSDSMGETDNPRLLSMNLENPS
	1		ļ	CNSVLDPRDLRQLHQMSSSSMSAGANSNTTVFVSQSDAFEGSD
ł	1		ì	FSCADNSMINESGPSNSTNPNSHGFVQDSQYSGIGSMQNEQLS
				DSFPYEFFQV
483	1222	1	1311	RRLSLLDLQLGPLGRDPPQECSTFSPTDSGEEPGQLSPGVQFQ
103	1222	1	1	RRONORRFSMEDVSKRLSLPMDIRLPQEFLQKLQMESPDLPKP
				LSRMSRRASLSDIGFGKLETYVKLDKLGEGTYATVFKGRSKLT
		Ì	İ	ENLVALKEIRLEHEEGAPCTAIREVSLLKNLKHANIVTLHDLI
				HTDRSLTLVFEYLDSDLKQYLDHCGNLMSMHNVKIFMFQLLRG
	}	İ		LAYCHHRKILHRDLKPONLLINERGELKLADFGLARAKSVPTK
			į	TYSNEVVTLWYRPPDVLLGSTEYSTPIDMWGVGCIHYEMATGR
1		İ		PLFPGSTVKEELHKINRLLGTPTEETWPGVTAFSEFRTYSFPC
	1			YLPQPLINHAPRLDTDGIHLLSSLLLYESKSRMSAEAALSHSY
		ł	ļ	FRSLGERVHQLEDTASIFSLKEIQLQKDPGYRGLAFQQPGRGK
1		İ		NRROSIF
484	1223	807	356	CTPHGSSSSWKIPLWPRHMSPLHSCLPVGTSTSSGPLAVPRDC
303		50,	550	FHLCCLWGQLLLISCPLACGQGCRVAGGQQHVPGQALGTLSPL
1	1			VSLLTWAGPSLDWPHPGSLVTPRCPILPAVPVLVKGLGGWPPT
1			ł	RPSRAAPVSGPWDQLPYFPGL
485	1224	1199	370	LISPVWGNIQRSRSVPLFPSGLVLGGIWARGPLLALLASFNII
303	1224	1199	3,3	SVLNAECYLKQILHPTSHFTVSETPPLSGNDTDSLSCDSGSSA
				TSTPCVSRLVTGHHLWASKNGRHVLGLIEDYEALLKQISQGQR
1	1	1		LLAEMDIQTQEAPSSTSQELGTKGPHPAPLSKFVSSVSTAKLT
				LEEAYRRLKLLWRVSLPEDGQCPLHCEQIGEMKAEVTKLHKKL
				FEQEKKLQNTMKLLQLSKRQEKVIFDQLVVTHKILRKARGNLE
				LRPGGAHPGTCSPSRPGS
L			J	TIME GOMIE GEOLORI GO

CCC	CEO	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	beginning	end	
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
1	Ì	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	<u> </u>	acid	acid	\=possible nucleotide insertion)
1		residue	residue	\=\text{possible flucteotide insertion}
	ļ	of amino	of amino	·
ŀ		acid	acid	·
		1	sequence	,
486	1225	sequence 2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECORO
400	1225	2403	1000	OLPVTFGNKOKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDR
	l	ļ ·	ļ	<del>-</del>
<b>[</b>		ĺ		EVVNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESR
Į.		ł	ŀ	WGYSGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIE
		ł	l .	YEKKQTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACA
	1			TLKGPDSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSI
İ		1		EDGQIPEIIFYT
487	1226	1193	372	SVWWNSEVKDWMQKKRRGLRNSRATAGDIAHYYRDYVVKKGLG
i				HNFVSGAVVTAVEWGTPDPSSCGAQDSSPLFQVSGFLTRNQAQ
			1	QPFSLWARNVVLATGTFDSPARLGIPGEALPFIHHELSALEAA
		1		TRVGAVTPASDPVLIIGAGLSAADAVLYARHYNIPVIHAFRRA
Į.				VDDPGLVFNQLPKMLYPEYHKVHQMMREQSILSPSPYEGYRSL
1	1	1		PRHOLLCFKEDCOAVFODLEGVEKVFGVSLVLVLIGSHPDLSF
1	į.	j	}	LPGAG\LTLQWILTSR
488	1227	756	1016	KLRPFIFSNOSLWLHSYEGAELEKTFIKGSWATFWVKVASCWA
400	122/	/30	1010	CVLLYLGLLLAPLCWPPTQKPQPLILRRRRHRIISPDNKYPPV
489	1228	1	747	QLIHLSHGYQIHWTDYYNVGTGRPEFGTRAAHKSLAGAELKTL
409	1228	-	/4/	KDFVTVLAKLFPGRPPVKKLLEMLQEWLASLPLDRIPYNAVLD
}		1		LVNNKMRISGIFLTNHIKWVGCQGSRSELRGYPCSLWKLFHTL
1	1	}	j	
	1			TVEASTHPDALVGTGFEDDPQAVLQTMRRYVHTFFGCKECGEH
			1	FEEMAKESMDSVKTPDQAILWLWKKHNMVNGRLAGEKPLGMGG
1		<u> </u>	<u> </u>	SARAEGGPGPGTARTARLPWGLSLSFAASCHPLC
490	1229	4797	2398	HGGATFINAFVTTPMCCPSRSSMLTGKYVHNHNVYTNNENCSS
1			i	PSWQAMHEPRTFAVYLNNTGYRTAFFGKYLNEYNGSYIPPGWR
		1	ļ	EWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKDYFTDLITNESI
}		Į.		NYFKMSKRMYPHRPVMMVISHAEPHGPEDSAPQFSKLYPNASQ
	1			HITPSYNYAPNMDKHWIMQYTGPMLPIHMEFTNILQRKRLQTL
				MSVDDSVERLYNMLVETGELENTYIIYTADHGYHIGQFGLVKG
I	1	ļ	1	KSMPYDFDIRVPFFIRGPSVEPGSIVPQIVLNIDLAPTILDIA
İ	Ì	1	1	GLDTPPDVDGKSVLKLLDPEKPGNRFRTNKKAKIWRDTFLVER
				GKFLRKKEESSKNIQQSNHLPKYERVKELCQQARYQTACEQPG
1	1			QKWQCIEDTSGKLRIHKCKGPSDLLTVRQSTRNLYARGFHDKD
1				KECSCRESGYRASRSQRKSQRQFLRNQGTPKYKPRFVHTRQTR
1				SLSVEFEGEIYDINLEEEEELQVLQPRNIAKRHDEGHKGPRDL
		1		QASSGGNRGRMLADSSNAVGPPTTVRVTHKCFILPNDSIHCER
1		1.		
	1			ELYQSARAWKDHKAYIDEEIEALQDKIKNLREVRGHLKRRKPE
1				ECSCSKQSYYNKEKGVKKQEKLKSHLHPFKEAAQEVDSKLQLF
	1			KENNRRRKKERKEKRRQRKGEECSLPGLTCFTHDNNHWQTAPF
ŀ			1	WNLGSFCACTSSNNNTYWCLRTVNETHNFLFCEFATGFLEYFD
	1			MNTDPYQLTNTVHTVERGILNQLHVQLMELRSCQGYKQCNPRP
ļ	1	1	j	KNLDVGNKDGGSYDLHRGQLWDGWEG
			<del></del>	<u></u>

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location '	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
,	i	to first	to first	Te infedime, vevalue, we repropried a relation
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
	ļ	residue	residue	
		of amino	of amino	
		acid	acid	
		sequence	sequence	THE TOTAL PRINCIPLE CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIEF CHIE
491	1230	2480	385	HLLIAQELADRVGEGRACWSLGNAYVSMGRPAQALTFAKKHLQ
				ISQEIGDRHGELTARMNVAQLQLVLGRLTSPAASEKPDLAGYE
		1		AQGARPKRTQRLSAETWDLLRLPLEREQNGDSHHSGDWRGPSR
			ļ	DSLPLPVRSRKYQEGPDAERRPREGSHSPLDSADVRVHVPRTS
	ł	ł	ŀ	IPRAPSSDEECFFDLLTKFQSSRMDDQRCPLDDGQAGAAEATA
	1	1	ł	APTLEDRIAQPSMTASPQTEEFFDLIASSQSRRLDDQRASVGS
	ļ			LPGLRITHSNAGHLRGHGEPQEPGDDFFNMLIKYQSSRIDDQR
		i		CPPPDVLPRGPTMPDEDFFSLIQRVQAKRMDEQRVDLAGGPGA
		ł	}	GGRRPARAPAAVPAWCELRPCAHRQAHPAPTPGRRSHSHSHVL
ĺ	l	1	1	PRPLPRTGTGHAAPRPPRPRATGSGQAARGGRACFHPGLAPMA
ł	1	ł	ĺ	LSFLPSAPAAGRTGPSACRPRPGAVRLPHPLPQALPVLPCPAK
		ł	1	CETLLSPSPSPKVSLSRLLGPPRTGPCSVPPELVLGWPCDRHA
1	1		Į.	PPLQLRPGAGLPPSLSPHSPARGQQPQKAPQTTHGRPGCSGSP
			ĺ	EVPPAESQGPAGASTGAGPISKAEGMAGHELRHSKTPSQEKGQ
			1	GLVLGMLTGSKSSAQSGWEVAPGSVTLTQVGGWSVEAGEASLS
Į		ļ	1	STLQTPHMRTPLLPPAGGDDITALSMGRGLTGHQVRDPRTGRT
]				CWSLRWAPGA
<u></u>	<del> </del>	<del> </del>	398	NSAADLAIFALWGLKPVVYLLASSFLGLGLHPISGHFVAEHYM
492	1231	3	398	FLKGHETYSYYGPLNWITFNVGYHVEHHDFPSIPGYNLPLVRK
		ł	1	IAPEYYDHLPQHHSWVKVLWDFVFEDSLGPYARVKRVYRLAKD
1	1	ĺ	1	1
	<u> </u>		1	GL
493	1232	1	214	QESGFSCKGPGQNVAVTRAHPDSQGRRRRPERGARGGQVFYNS
ļ	1	1		EYGELSEPSEEDHCSPSARVTFFTDNSY
494	1233	3	443	VIVHARPIRTRASKYYIPEAVYGLPAYPAYAGGGGFVLSGATL
	1	1	<b>,</b>	HRLAGACAQVELFPIDDVFLGMCLQRLRLTPEPHPAFRTFGIP
	1	1	1	QPSAAPHLSTFDPCFYRELVVVHGLSAADIWLMWRLLHGPHGP
	1		1	ACAHPQPVAAGPFQWDS
495	1234	1	897	MASAACSMDPIDSFELLDLLFDRQDGILRHVELGEGWGHVKDQ
			1	VLPNPDSDDFLSSILGSGDSLPSSPLWSPEGSDSGISEDLPSD
	1		1	PODTPPRSGPATSPAGCHPAQPGKGPCLSYHPGNSCSTTTPGP
ŀ	1			VIOOOHHLGASYLLRPGAGHCQELVLTEDEKKLLAKEGITLPT
1				QLPLTKYEERVLKKIRRKIRNKQSAQESRKKKKEYIDGLETRS
1				CCCPLPSSSSPPSALLAPTKPRALGTLRLYECSPELCTTMLPP
				AWLLMLCQAPRPQDPDPRLTQPEKSLQEAPGQTGASRTPRT
i	l	l		WATELING AUTE COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLO

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
		sequence	sequence	
496	1235	4235	940	ARGRRSRPVWAASWGGRGRPAARRRPRGLAATMGFELDRFDGD VDPDLKCALCHKVLEDPLTTPCGHVFCAGCVLPWVVQEGSCPA RCRGRLSAKELNHVLPLKRLILKLDIKCAYATRGCGRVVKLQQ LPEHLERCDFAPARCRHAGCGQVLLRRDVEAHMRDACDARPVG RCQEGCGLPLTHGEQRAGGHCCARALRAHNGALQARLGALHKA LKKEALRAGKREKSLVAQLAAAQLELQMTALRYQKKFTEYSAR LDSLSRCVAAPPGGKGEETKSLTLVLHRDSGSLGFNIIGGRPS VDNHDGSSSEGIFVSKIVDSGPAAKEGGLQIHDRIIEVNGRDL SRATHDQAVEAFKTAKEPIVVQVLRRTPRTKMFTPPSESQLVD TGTQTDITFEHIMALTKMSSPSPPVLDPYLLPEEHPSAHEYYD PNDYIGDIHQEMDREELELEEVDLYRMNSQDKLGLTVCYRTDD EDDIGIYISEIDPNSIAAKDGRIREGDRIIQINGIEVQNREEA VALLTSEENKNFSLLIARAELQLDEGWMDDDRNDFLDDLHMDM LEEQHHQAMQFTASVLQQKKHDEDGGTTDTATILSNQHEKDSG VGRTDESTRNDESSEQENNGDDATASSNPLAGQRKLTCSQDTL GSGDLPFSNKSFISPECTGAAYLGIPVDECERFRELLELKCQV KSATPYGLYYPSGPLDAGKSDPESVDKELELLNEELRSIELEC LSIVRAHKMQQLKEQYRESWMLHNSGFRNYNTSIDVRRHELSD ITELPEKSDKDSSSAYNTGESCRSTPLTLEISPDNSLRRAAEG ISCPSSEGAVGTTEAYGPASKNLLSITEDPEVGTPTYSPSLKE LDPNQPLESKERRASDGSRSPTPSQKLGSAYLPSYHHSPYKHA HIPAHAQHYQSYMQLIQQKSAVEYAQSQMSLVSMCKDLSSPTP SEPRMEWKVKIRSDGTRYITKRPVRDRLLRERALKIREERSGM TTDDDAVSEMKMGRYWSKEERKQHLVKAKEQRRRREFMMQSRL DCLKEQQAADDRKEMNILELSHKKMMKKRNKKIFDNWMTIQEL LTHGTKSPDGTRVYNSFLSVTTV
497	1236	2	157	FFFLVEMGFCHVGQGGLTLIGSSNLPASASKSAGITGVSHCAR PDFKSCVE
498	1237	1	211	LAGRKVLLFVSGYVVGWGPITWLLMSEVLPLRARGVASGLCVL ASWLTAFVLTKSFLPGGVSVQPQAPGP
499	1238	2	345	FWAPGPPGVGAAVGDASTRSLRESCPSPSPGRLRRTTAPWSSQ ARAAAPAPSSSCRGPDGASSPRDLPWRPWKILRRTPLSGDVEL SQVHPDQRILRRFILSRTCGNTIPGMAE
500	1239	1	523	MRRFLSKVYSFPMRKLILFLVFPVVRQTPTQHFKNQFPALHWE HELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECS BIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCEVGS NWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAF LL

CEC	CEC	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	beginning	end	Amino acid segment containing signal peptide (A—Aranine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of Nucleic	of	согге-	согте-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1		acid	acid	\=possible nucleotide insertion)
		residue	residue	1-possible medecide institution
İ		of amino	of amino	
		acid	acid	
l	ŀ	sequence	sequence	
501	1240	2	1277	FVWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHY
	ļ	l	1	AGQDATDPFVAFHINKGLVKKYMNSLLIGELSPEQPSFEPTKN
		ĺ	[	KELTDEFRELRATVERMGLMKANHVFFLLYLLHILLLDGAAWL
	ŀ	1	1	TLWVFGTSFLPFLLCAVLLSAVQAQAGWLQHDFGHLSVFSTSK
		ł		WNHLLHHFVIGHLKGAPASWWNHMHFQHHAKPNCFRKDPDINM
			ŀ	HPFFFALGKILSVELGKOKKKYMPYNHOHKYFFLIGPPALLPL
	Ì	1	1	YFOWYIFYFVIORKKWVDLAWMITFYVRFFLTYVPLLGLKAFL
	1			GLFFIVRFLESNWFVWVTQMNHIPMHIDHDRNMDWVSTQLQAT
			1	CNVHKSAFNDWFSGHLNFQIEHHLFPTMPRHNYHKVAPLVQSL
İ		1		CAKHGIEYQSKPLLSAFADIIHSLKESGQLWLDAYLHQ
	1		540	OCGGIPYNTTQFLMNDRDPEEPNLDVPHGISHPGSSGESEAGD
502	1241	999	540	SDGRGRAHGEFQRKDFSETYERFHTESLQGRSKQELVRDYLEL
i		l	ľ	
1		Į.		EKRLSQAEEETRRLQQLQACTGQQSCRQVEELAAEVQRLRTEN
	<u> </u>		<u> </u>	QRLRQENQMWNREGCRCDEEPGT
503	1242	1448	875	SPERSSLSVGREKAMEVPPPAPRSFLCRALCLFPRVFAAEAVT
1				ADSEVLEERQKRLPYVPEPYYPESGWDRLRELFGKD\VTGSLF
1 .			1	RINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYSGETVQERKQ
Į.	ļ			KDRKALHELKLEEWKGRLQVTEHLPEKIESSLQEDEPENDAKK
	1	1		IEALLNLPRNPSVIDKQDKD
504	1243	149	1293	RSLGLAVTEMVPWVRTMGQKLKQRLRLDVGREICRQYPLFCFL
		[		LLCLSAASLLLNRYIHILMIFWSFVAGVVTFYCSLGPDSLLPN
	ļ	1		IFFTIKYKPKQLGLQELFPQGHSCAVCGKVKCKRHRPSLLLEN
1	1	1		YQPWLDLKISSKVDASLSEVLELVLENFVYPWYRDVTDDESFV
		1	1	DELRITLRFFASVLIRRIHKVDIPSIITKKLLKAAMKHIEVIV
	1	Ì	i	KARQKVKNTEFLQQAALEEYGPELHVALRSRRDELHYLRKLTE
				LLFPYILPPKATDCRSLTLLIREILSGSVFLPSLDFLADPDTV
1				NHLLIIFIDDSPPEKATEPASPLVPFLQKFAEPRNKKPSVLKL
	1	1		ELKQIREQQDLLFRFMNFLKQEGAVHVLHVLFDCGGI
505	1244	2	1116	QSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLV
1 -00		-	]	NHYMKGGFYPRGVTSEIAFHTIPVIQRAGGAVLTKATVQSVLL
				DSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNA
1				RCLPGVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVY
1	1			YDTDMDQAMERYVSMPREEAAEHIPLLFFAFPSAKDPTWEDRF
1	1			PGRSTMIMLIPTAYEWFEEWQAELKGK\RGSDYETFKNSFVEA
1				SMSVVLKLFPQLEGKVESVTAGSPLTNQFYL\AAPRGACYGAD
1	1			HDLGRLHPCVMASLRAQSPIPNLYLTGQDIFTCGLVGALQGAL
		1		l ·
	4	L	1	LCSSTILKRNLYSDLKNLDSRIRAQKKKN
506	1245	1759	873	RPQETRVLQVSCGRAHSLVLTDREGVFSMGNNSYGQCGRKVVE
1	1	1		NEIYSESHRVHRMQDFDGQVVQVACGQDHSLFLTDKGEVYSCG
1		1		WGADGQTGLGHYNITSSPTKLGGDLAGVNVIQVATYGDCCLAV
				SADGGLFGWGNSEYLQLASVTDSTQVNVPRCLHFSGVGKVRQA
	ł	1		ACGGTGCAVLNGEGHVFVWGYGILGKGPNLVESAVPEMIPPTL
1	1			FGLTEFNPEIQVSRIRCGLSHFAALTNKGELFVWGKNIRGCLG
	1	1		IGRLEDQYFPWRVTMPGEPVDVACGVDHMVTLAKSFI
L	_1			

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
507	1246	sequence 520	sequence 2	LPFREWLMIVVSLSAAAVAAAFMAKCRMVLSSRYFCSHFVMSA SRARIRSSFSRTSSRRAGALYSGMLAGWPFPCFCWVLSASSSL SSQVRSLRSICSRFSHADCSWVRACCSFSTFSTYACFSRNSSS SLMTLAWALLKAWSRISMCLRWSSLAVRTAANSISNFSFSFKN
508	1247	1	1083	MQAVRATASQSLSCARAPREPTQHALRAHWFPPAAAVQPSPHS GVAAAAGTWSSAFRGEHPLVSSGLLLGVREQSFRLLRSKAGTH MYLEHTSHCPHHDDDTAMDTPLPRPRPLLAVERTGQRPLWAPS LELPKPDMQPLPAGAFLEEVAEGTPAQTESEPKVLDPEEDLLC IAKTFSYLRESGWYWGSITASEARQHLQKMPEGTFLVRDSTHP SYLFTLSVKTTRGPTNVRIEYADSSFRLDSNCLSRPRILAFPD VVSLVQHYVASCTADTRSDSPDPAPTPALPMPKEDAPSDPALP APPPATAVHLKLVQPFVRRSSARSLQHLCRLVINRLVADVDCL PLPRRMADYLRQYPFQL
509	1248	2	841	FVDIFQRWKECRGKSPAQAELSYLNKAKWLEMYGVDMHVVRGR DGCEYSLGLTPTGILIFEGANKIGLFFWPKITKMDFKKSKLTL VVVEDDDQGREQEHTFVFRLDSARTCKHLWKCAVEHHAFFRLR TPGNSKSNRSDFIRLGSRFRFSGRTEYQATHGSRLRRTSTFER KPSKRYPSRRHSTFKASNPVIAAQLCSKTNPEVHNYQPQYHPN IHPSQPRWHPHSPNVRPSFQDDRSHWKASASGDDSHFDYVHDQ NQKNLGGMQSMMYRDKLMTAL
510	1249	2	763	GGIRLIQKLTWRSRQQDRENCAMKGKHKDECHNFIKVFVPRND EMVFVCGTNAFNPMCRYYRVSIFYVICFF*STFLPSLICC*S* NLSAFQ*FVLSLVQ*KNKDRILQMEF*YK*NSIAFKRAR*IDM TLAIYFSFV\LSTL*YDGEEISGLARCPFDARQTNGALFADGK LYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWIKE/PHFL YAIK/Y/GNYVYFSFREIVAT**LG/KAVDS/RVARYEKQLVG PTV
511	1250	1555	629	ARALARERESESARADDVTLGVSAILAVDRGGNLGSA\DGWAY IDVEVRRPWAFVGPGCSRSSGNGSTAYGLVGSPRWLSPFHTGG AVSLPRRPRGPGPVLGVARPCLRCVLRPE\HYEPGSHYSGFAG RDASRAFVTGDCSEAGLVDDVSDLSAAEMLTLHNWLSFYEKNY VCVGRVTGRFYGEDGLPTPALTQVEAAITRGLEANKLQLQEKQ TFPPCNAEWSSARGSRLWCSQKSGGVSRDWIGVPRKLYKPGAK EPRCVCVRTTGPPSGQMPDNPPHRNRGDLDHPNLAEYTGCPPL AITCSFPL
512	1251	1100	798	YFIICRDGVLLFCPGWSQTPGAQAILLHWATQNAGMTDMSHSA QPIYLFIYLIRTRSHYVAQAGQLLDSNDSPNVASQNVGITGMS HHAWLKIVLYFCII

SEQ SEQ Predicted beginning and nucleotide location of of location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location location	Alanine,
NO: NO: nucleotide nucleotide   C=Cystelle, B=Aspathe Acte, B=Statistic New   No:   nucleotide   nucleotide   F=Phenylalanine, G=Glycine, H=Histidine, I=Is	
NO: NO: location location   F=Phenylalanine, G=Glycine, H=Histidine, I=Is	
	oleucine,
N=Lysille, L=Leucille, lyi-lyicullollille, ly-Aspa	
Nucleic Amino Control P=Proline Q=Glutamine R=Arginine S=Sering	
Acids   Acids   sponding   sponding   P=Proline, Q=Glutamine, R=Arginine, S=Sering   T=Threonine, V=Valine, W=Tryptophan, Y=Ty	
amino amino X=Unknown, *=Stop Codon, /=possible nucleoti	
	de deletion,
acid acid \=possible nucleotide insertion)	
of amino of amino	
acid acid	
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	
sequence   sequence	ARGSSDDA
RPAPAMVRPRRAPYRSGAGGPLGGRGRPPRPLVVR	
ASPRGPQPPR\IRARSAPPMEGARVFGALGPIGPS	
LAVSEHRLSNKLLAWSGVLEWQEKRRPYSDSTAKL	
YVNOGENLETDQWPQKLIMQLIPQQLLTTLGPLFR	
, , , , , , , , , , , , , , , , , , , ,	
FTNRDCDSLKGLCRIMGNGFAGCMLFPHISPCEVR	
KKKIFMGLIPYDQSGFVSAIRQVITTRKQAVGPGG	
VNNKFLAWSGVMEWQEPRPEPNSRSKRWLPSHVYV	
EQWPRKLYMQLIPQQLLTTLVPLFRNSRLVQFHFT	
LCRIMDNGFAGCVHFSYKASCEIRVLMLLYSSEKK	
DQGNFVNGIRRVIANQQQVLQRNLEQEQQQRGMGG	
514 1253 320 964 GRPALGREAPPQAGLSSTPPPCSETCTMGPHSILR	
TPPEPSAEPHPLSLLTSSNTSLAGTSLGRDLTPGG	
PRNPESPRHRLGSPRGRRWLASPTPTGSGRSGPAS	
AAQDPTSEGASVGAMEAGLGPPTAAPRGVVSEAAE	SLGGTLSW
GAWGRPPAGPSGLAGRRSRREALRPDRKEASVMMA	
515 1254 704 107 PGVPTHGWPRSRVLTRVRGSRGSGKMAAAVVLAAG	LRAARRAV
AATGVRGGQVRGAAGVTDGNEVAKAQQATPGGAAP	
KSLPADILYEDQQCLVFRDVAPQAPVHFLVIPKKP	
EEDQQ/LTYVPPLSL*LLGHLLLVAKQTAKAEGLG	DGYRLVIN
DGKLGAQSVYHLHIHVLGGRQLQWPPG	
516 1255 2299 924 VPNYLPSVSSAIGGEVPQRYVWRFCIGLHSAPRFL	
YLSCTSPCSCYRPLCRLNFGLNVVENLALLVLTYV	
WVPG*GRSGEVFPEGTGLPLPHSDLPTSWCGHSLQ	CGSQSSFP
PAIHENAFIVFIASSLGHMLLTCILWRLTKKHTVS	QE\DGLSL
AGAPRQPRRKSRTSVLRIRVMVRWELSSNGNPGRG	VLGLGLGL
GNKLRVVGQNLGL*HCVWVVWETGE*KRWRLQMGI	E*GVASRR
Q*VRNSVRGLVCHNSSAPPMYMGFFSPTVFGGGVG	G*LHVTFI
LHPPEVEAAGIPLLLGPSLPQRQGREHIVVILAAP	
*WEPREIRPSP*ELGLRGEPTLSYPASCRVIRQPI	P*DRKSYS
WKQRLFIINFISFFSALAVYFRHNMYCEAGVYTIF	AILEYTVV
LTNMAFHMTAWWDFGNKELLITSQPEEKRF	
517 1256 3 254 IDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAY	LKKEFEKH
GAVVNESHHDALVEDIFDKEDEDKDGFISAREFTY	
518 1257 2 611 PRVRGRVGKEGAAAKPRSLLRRFQLLSWSVCGGNK	
SCLDLKECGHAYSGIVAHQKHLLPTSPPISQASEG	
AOMLLSTLOSTORPTLPVGSLSSDKELTRPNETTI	
AGPEAGENQKQPEKNAGPTARTSATVPVLCLLAII	
YVLCKRRRGQSPQSSPDLPVHYIPVAPDSNT	
	SOYRKEDE
519 1258 1002 418 LIISNFLKAKQKPGSTPNLQQKKSQARLAPDIVSA FQTGILIYELLHQPNPFEVRAQLRERDYRQEDLPF	
PGLQQLAHLLLEADPIKRIRIGEAKRVLQCLLWGF	מיטטוי זמממי
GTSEEALCGTLHNWIDMKRALMMKFAEKAVDRRF	CASTEDAT
CCQYLASAEPGALLQSLKLLQLL	

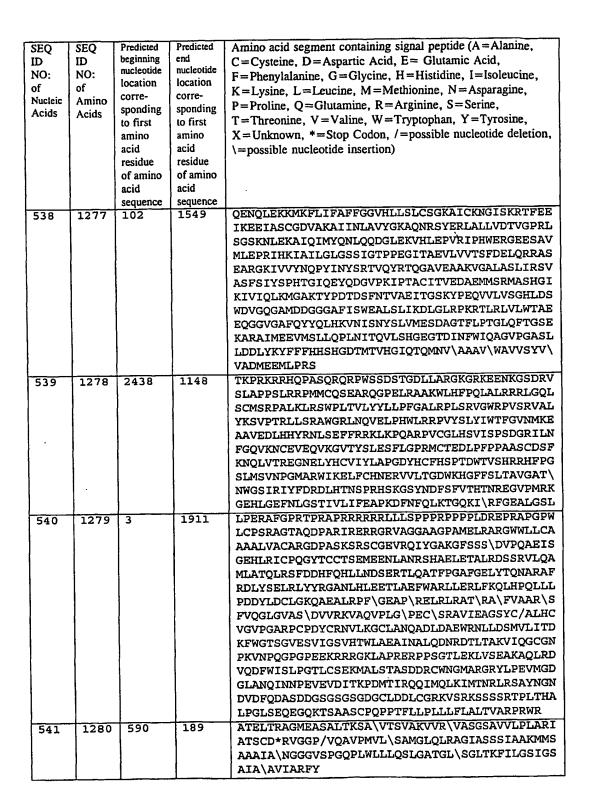
SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID I	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		to first	to first	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		amino	amino acid	
		acid residue	residue	\=possible nucleotide insertion)
Ì		of amino	of amino	
		acid	acid	
1		sequence	sequence	·
520	1259	2	2019	KRGLIVVMAHEMIGTQIVTERGVALLESGTEKVLLIDSRPFVE
320	1233	_	2022	YNTSHILEAININCSKLMKRRLQQDKVLITELIQHSAKHKVDI
1			į	DCSQKVVVYDQSSQDVASLSSDCFLTVLLGKLEKSFNSVHLLA
ļ		l	1	GGFAEFSRCFPGLCEGKSTLVPTCISQPCLPVANIGPTRILPN
	ł		}	LYLGCQRDVLNKELMQQNGIGYVLNASNTCPKPDFIPESHFLR
		l		VPVNDSFCEKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRS
	İ		İ	ATIAIAYIMKRMDMSLDEAYRFVKEKRPTISPNFNFLGQLLDY
1	Ì	}		EKKIKNOTGASGPKSKLKLLHLEKPNEPVPAVSEGGQKSETPL
	İ		Ì	SPPCADSATSEAAGQRPVHPASVPSVPSVQPSLLEDSPLVQAL
1		Ì		SGLHLSADRLEDSNKLKRSFSLDIKSVSYSASMAASLHGFSSS
		ļ		EDALEYYKPSTTLDGTNKLCQFSPVQEL/CGADSRNQS**GGS
ĺ		ì	ļ	Q/PSPRSCRPPGLQTARASDCIRSEPAAVAPPRGPFYLHCIEV
		ļ		GAWRTITTPASFSAFPP\PAAPHEVCWPGP*GLA\PDILAPQT
	1	ĺ		STPSLTSSWYFATESSHFYSASAIYGGSASYSAYSCSQLPTCG
	1	ļ		DQVYSVRRRQKPSDRADSRRSWHEESPFEKQFKRRSCQMEFGE
		1		SIMSENRSREELGKVGSQSSFSGSMEIIEVS
521	1260	20	803	ASSSKRVSRQKMLQLWKLVLLCGVLTGTSESLLDNLGNDLSNV
341	1200	20	***	VDKLEPVLHEGLETVDNTLKGILEKLKVDLGVLQKSSAWQLAK
			İ	OKAQEAEKLLNNVISKLLPTNTDIFGLKISNSLILDVKAEPID
	İ	İ	ł	DGKGLNLSFPVTANVTEAGPIIDQIIN\LRASLDLLTAVTIET
1	ŀ	1	1	DPQTHHPVAGLGECARDPTSISLCLLDKHSQIINKFVNSVINT
1	1	i		LKSTVSSLLQKEICPLIRIFIHSLDVNVIQQVVDNPQHKTQLQ
1			1	TLI
522	1261	1246	411	CSLRRPRSAAEPDADHVPLLGLLRLQLRAARQPGAMRPQGPAA
322	1201	1240		SPORLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLY
	i			NGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECL
	1		Į	RESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSAL
	Ĭ	ļ	1	RVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ
		i		GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPK
1	1	į.	Ì	GDASTGWNSVSRIIIEELPK
523	1262	2009	921	MHSAMLGTRVNLSVSDFWRVMMRVCWLVRQDSRHQRIRLPHLE
523	1202	2009	12.1	AVVIGRGPETKITDKKCSRQQVQLKAECNKGYVKVKQVGVNPT
	1			SIDSVVIGKDQEVKLQPGQVLHMVNELYPYIVEFEEEAKNPGL
1 .	1			ETHRKRKRSGNSDSIERDAAQEAEAGTGLEPGSNSGQCSVPLK
1	1		1	KGKDAPIKKESLGHWSQGLKISMQDPKMQVYKDEQVVVIKDKY
1	1			PKARYHWLVLPWTSISSLKAVAR\EHLELLKHMHTVGEKVIVD
1	1		1	FAGSSKLRFRLGYHAIPSMSHVHLHVISQDFDSPCLKNKKHWN
1	1			SFNTEYFLESQAVIEMVQEAGRVTVRDGMPELLKLPLRCHECQ
1	1			QLLPSIPQLKEHLRKHWTQ
				Anny o te Aniversation - A

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
524	1263	2067	198	DMSDTSESGAGLTRFQAEASEKDSSSMMQTLLTVTQNVEVPET PKASKALEVSEDVKVSKASGVSKATEVSKTPEAREAPATQASS TTQLTDTQVLAAENKSLAADTKKQNADPQAVTMPATETKKVSH VADTKVNTKAQETEAAPSQAPADEPEPESAAAQSQENQDTRPK VKAKKARKVKHLDGEEDGSSDQSQASGTTGGRRVSKALMASMA RRASRGPIAFWARRASRTRLACFGPGEPLLSPWRSP\KARRQR GFAVRVAKFQ\SSQEPEAPPPW\DVALLQGRAN\DLVKYLLAK DQTKIPIKRS\DMLKDIIKEYTDVYPEII\ERAGYSLE\KVFG IQLKEIDKNDHLYILLSTLEPTDAGILGTTKDSPKLGLLMVLL SIIF\MNGNRS\SEAVIWEVLR\RSLGLRLGIHHS\LLGDVK\ KLITDEV\VKQKYL\DYARVPHSNSP\EYEFFWG\LRSYYEDQ QR*KSFKFACK\VQK\KDPK\EWAAQSPPGKAR\ERMEAD\LK AAS*GSPWKPRLRAEIKARMGIGLGSENAAGPCNWDEADIGPW AKARIQAGAEAKAKAQESGSASTGASTSTNNSASASASTSGGF SAGASLTATLTFGLFAGLGGAGASTSGSSGACGFSYK
525	1264	1	1397	ARPPVCTGSTMSLTVVSMACVGFFLLQGAWPLMGGQDKPFLSA RPSTVVPRGGHVALQCHYRRGFNNFMLYKEDRSHVPIFHGRIF QESFIMGPVTPAHAGTYRCRGSRPHSLTGWSAPSNPLVIMVTG NHRKPSLLAHPGPLLKSGETVILQCWSDIMFEHFFLHKEGISK DPSRLVGQIHDGVSKANFSIGPMMLALAGTYRCYGSVTHTPYQ LSAPSDPLDIVVTGPYEKPSLSAQPGPKVQAGESVTLSCSSRS SYDMYHLSREGGAHERRLPAVRKVNRTFQADFPLGPATHGGTY RCFGSFRHSPYEWSDPSDPLLVSVTGNPSSSWPSPTEPSSKSG NLRHLHILIGTSVVKIPFTILLFFLLHRWCSNKK\NAAVMDQE PAGNR\VNSEDSDEQDHQEVSYP*LEHCVFTQRKITRPSQRPK TPPTDTSMYIELPNAEPRSKVVFCPRAPQSGLEGIF

C-000	050	Donding	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	Predicted beginning	end	Amino acid segment containing signal peptide (A—Alamine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of .	corre-	согге-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
	i	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
	Ì	residue	residue	- possioic indocesses insertion,
		of amino	of amino	
1		acid	acid	
į		sequence	sequence	· · · · · · · · · · · · · · · · · · ·
526	1265	6657	988	LHNLRERYFSGLIYTYSGLFCVVVNPYKHLPIYSEKIVDMYKG
320	1205	1 3337		KKRHEMPPHIYAIADTAYRSMLQDREDQSILCTGESGAGKTEN
į.		ļ	1	TKKVIQYLAVVASSHKGKKDTSITGELEKQLLQANPILEAFGN
	1	1		AKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEKSRAIR
				QARDERTFHIFYYMIAGAKEKMRSDLLLEGFNNYTFLSNGFVP
	1			IPAAQDDEMFQETVEAMAIMGFSEEEQLSILKVVSSVLQLGNI
	1			VFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIK
	1	1		VGRDVVQKAQTKEQADFAVEALAKATYERLFRWILTRVNKALD
1		1	ł	KTHROGASFLGILDIAGFEIFEVNSFEQLCINYTNEKLQQLFN
	1	1	l	HTMFIL\EQEEYQREGIEWNFIDFGLDLQPCIELIERPNNPPG
	Į.	Į.	ļ	VLALLDEECWFPKATDKSFVEKLCTEQGSHPKFQKPKQLKDKT
	1	l		EFSIIHYAGKVDYNASAWLTKNMDPLNDNVTSLLNASSDKFVA
1	İ		1	EFSTIHYAGKVDYNASAWETKNINDPENDINVISBENASSDAFVA
			1	DLWKDVDRIVGLDQMAKMTESSLPSASKTKKGMFRTVGQLYKE
	1		1	QLGKLMTTLRNTTPNFVRCIIPNHEKRSGKLDAFLVLEQLRCN
		}	ì	GVLEGIRICRQGFPNRIVFQEFRQRYEILAANAIPKGFMDGKQ
			i	ACILMIKALELDPNLYRIGQSKIFFRTGVLAHLEEERDLKITD
1.	1 .	ł	ì	VIMAFQAMCRGYLARKAFAKRQQQLTAMKVIQRNCAAYIKLRN
1			İ	WQWCRLFTKV*PLLQVTRQE*EMQAKEDELQKTKERQQKAENE
1		ì		LKELEQKHSQLTEEKNLLQEQLQAETELYAEAEEMRVRLAAKK
1		1	1	QELEEILHEMEARLEEEEDRGQQLQAERKKMAQQMLDLEEQLE
		1	ŀ	EEEAARQKLQLEKVTAEAKIKKLEDEILVMDDQNNKLSKERKL
i	1	1		LEERISDLTTNLAEEEEKAKNLTKLKNKHESMISELEVRLKKE
		1		EKSRQELEKLKRKLEGDASDFHEQIADLQAQIAELKMQLAKKE
	Ì		1	EELQAALARLDDEIAQKNNALKKIRELEGHISDLQEDLDSERA
	j		}	ARNKAEKQKRDLGEELEALKTELEDTLDSTATQQELRAKREQE
1	1			VTVLKR\ALNEETRSHEAQVQEMRQKHAQAVQSLTEQLEQ*K
1	1	ļ	1	RAKANLDKNKQTLEKENTD\LAGELRVLGQA\KQEVEHRMKKL
	1	1	1	QAQVQELQSKCSDGERARAELNDKVHK\LQNEVESVTG\MLNE
		1	į	AEGKAIKLAKDVASLSSQL\QDTQELLQEESRQKLNVST\SLR
ļ	1	İ		\QLEEERNSLQDQLDEEMEAKQNLERHISTLNIQLSDSKKKLQ
į.		1		DFASTVEALEEGKKRFQKEIENLTQQYEEKAAAYDKLEKTKNR
	1			LOQELDDLVVDLDNQRQLVSNLEKKQRKFDQLLAEEKNISSKY
		1		ADERDRVEAEAREKETKALSL\ARALEEALEAKEELERTNKML
	[			KA\EMGRPGSASKD\DVGQELSHDL\EKSK\RALGDPRLEEMK
	1	1	1 .	T\QLEELGRTELASPRRDA\KLRLEVNMQAPSRASFER\DLQA
1	ļ	1		RTEQNE\ESRR\HLQRQLHEYETELEDERKQRALAAAAKIKLG
				WDPVRTLDL*ADSAIKGRGGKAIKQLRKLQAQMKDFQRELEDA
1				\RASRDEIF\ATA\KENEKKAKSLEA\DLMQLQE\DLAAAEEG
		1	1	RKQ\ADLE\KEELAEEL\ASSLSGRNALQDEKRRLEARIAQLE
	1		1	RKQ\ADLE\REELAEEL\ASSISGRNALQDERRREARTAQIS EELEEEQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKNES
		1	Ī	EELEEQGNMEAMSDKVKKAIQQAEQUSNEUAIEKSIAQKNES
1				ARQQLERQNKELRSKLHEMEGAVKSKFKSTIAALEAKIAQLEE
Ì	1			QVEQEAREKQAATKSLKQKDKKLKEILLQVEDERKMAEQYKEQ
	1			AEKGNARVKQLKRQLEEAEEESQRINANRRKLQRELDEATESN
1			1	EAMGREVNALKSKLRRGNETSFVPSRRSGGRRVIENADGSEEE
	1			TDTRDADFNGTKASE
<del></del>				

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	i i	acid	acid	\=possible nucleotide insertion)
		residue	residue	(=possible flucteoride first troit)
1	ĺ	of amino	of amino	
		acid	acid	
•		sequence	sequence	
527	1266	1	775	KLHFAKSLNSELSCSTREAMQDEDGYITLNIKTRKPALVSVGP
]		-		ASSSWWRVMALILLILCVGMVVGLVALGIWSVMQRNYLQDENE
ļ		t		NRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYG
				DSCYGFFRHNLTWEESKQYCTDMNATLLKIDNRNIVEYIKAR\
				THLIRWVGLSRQKSNEVWKWEDGSVISENMFEFLEDGKGNMNC
1		1		AYFHNGKMHPTFCENKHYL\MCE\RKAGHDPRWTQLPLMPKRW
			ļ	TG .
528	1267	1053	424	NQGLRDVGLCRTCLVNKIFASSILGKSHHHSLVSINQGHNAPW
328	1207	1033	727	KAAGS\LPLKAAYC\QGFSPCDCLKYG\SWDEKDLMVPQPDTH
1		1		KGSVLRWISKRGKPLAVEMEEGHCL\CLPLGTECLGVKP\IVH
ļ				LFNSEMGEK\RPVAG\ARHVGSSAALLFFTPLRCLGGEKHKSG
1		1		LRARPGIVPSLELNYDIDSFAHMFF/SVDLLLIITLLSYYIPF
ļ	İ	ł		C
			1560	MWWRLAPTQAIWRAAGCCMRFSRRRSTCCCLASCIFLLYKIVR
529	1268	1435	1200	GDOPAAKRORRRAAPSAPPQAARLHPPPKLRRFDGVQDPAP
Ì		1		YSWAINGKVFDVTQRPANFLRGPRGPETLSDWESQFTFKYHHV
		1	İ	GKLLKEGEEPTVYSDEEEPKDESARKND*
<u>.</u>				GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCL
530	1269	705	166	GASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPK
			1	KEILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDL
			1	FRE\ADIEPNGKVKYDEFIHKI/TLLPGRDLLKEENGRASPGP
1	1			· ·
L	ļ	<u> </u>	· ·	ENLEQLIFL
531	1270	25	1396	ADPHTTVIRFFPAASATKRVLPPVLRVSSPRTWNPNVPESPRI
	ļ		1	PAPRLPKRMSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRF
)	}		j	ASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGS
				ACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFH
			Į.	KVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKR
i	}	ļ	1	LPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFEIQPQ
Į	İ			GSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGD
İ				PHGEFWLGLEKVHSITGDRNSRLAVQLRDWDGNAELLQFSVHL
1			1	GGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQDHDLR
		1	ĺ	RDKNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIF
			İ	WKTWRGRYYPLQATTMLIQPMAAEAAS
532	1271	1276	90	ALDFGDSCQWPRPQDTMKQLPVLEPGDKPRKATWYTLTVPGDS
	-			PCARVGHSCSYLPPVGNAKRGKVFIVGGANPNRSFSDVHTMDL
1	1	1		GKHQWDLDTCKGLLPRYEHASFIPSCTPDRIWVFGGANQSGNR
1	1		}	NCLQVLNPETRTWTTPEVTSPPPSPRTFHTSSAAIGNQLYVFG
	1	1		GGERGAQPVQDTKLHVFDANTLTWSQPETLGNPPSPRHGHVMV
1	1		1	AAGTKLFIHGGLAGDRFYDDLHCIDISDMKWQKLNPTGAA\PA
	1			GCAS/HTPAVAMGK\HVYI\FGGMTPAGAPGTQCTQYHTEEQH
				WDPCLKF\DTPSYPPGTIGTHSHVVSFPW\PVTCASEKEDS\N
				SLTLNHEAEKEDSADKVMSHSGDSHEESQTATLLCLVFGGMNT
}				EGEIYDDCIVTVVD
	1	_1		202120011110

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end mucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  GFSIGKATDRMDAFRKAKNRAVHHLHYIERYEDHTIFHDISLR
533	1272	1169	639	FKRTHIKMKKQPKGYGLRCHRAIITICRLIGIKDMYAKVSGSI NMLSLTQGLFRGLSRQETHQQLADKKGLHVVEIREECGPLPIV VASPRGPLRKDPEPEDEVPDVKLDWEDVKTAQGMKRSVWSNLK RAAT
534	1273	25		ADPHTTVIRFFPAASATKRVLPPVLRVSSPRTWNPNVPESPRI PAPRLPKRMSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRF ASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGS ACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLFH KVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKR LPEMAQPVDPAHNVSRLHRLPRDCQELFQVGERQSGLFEIQPQ GSPPFLVNCKMTSDGGWTVIQRRHDGSVDFNRPWEAYKAGFGD PHGEFWLGLEKVHSITGDRNSRLAVQLRDWDGNAELLQFSVHL GGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQDHDLR RDKNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIF WKTWRGRYYPLQATTMLIQPMAAEAAS
535	1274	. 23	1102	TLRSRPAGEAGYLGWDPEQAGEGSALSRPGAMAALMTPGTGAP PAPGDFSGEGSQGLPDPSPEPKQLPELIRMKRDGGRLSEADIR GFVAAVVNGSAQGAQIGAWGGLGVPDPDWEVSPRDFGSLGVRR CPTTSTGPRVPHRCGLPPSRVPPHTRG\MLMAIRLRGMDLEET SVLTQALAQSGQQLEWPEAWRQQLVDKHSTGGVGDKVSLVLAP ALAACGCKVINHLLSRREPIPHMQQPVHPQAAPNLKPGPKPPR PYQGFSPPCSPAQFSPPRSPAQRLGPLWLQTRPLGAGKRSTDG IQTPFPLGPQTAPPREELRTSLPLPQALFPQGQVPTSSPTDTS QPRKLPFHSLTSWAPL
536	1275	3	439	RALRELRERVTHGLAEAGRDREDVSTELYRALEAVRLQNSEGS CEPCPTSWLPFGGSCYYFSVPKTTWAEAQGHCADASAHLA/IV GGLGEQDFLSRDTSALEYWIGRRAVQHLRKVQGYSWVDGVPLS FR*/WEG/HPGETWGPQVRL
537	1276	1	564	RWPRSWPPRAGAARGAAEAAMVGALCGCWFRLGGARPLIPLGP TVVQTSMSRSQVALLGLSLLLMLLLYVGLPGPPEQTSCLWGDP NVTVLAGLTPGNSPIFYREVLPLNQAHRVEV\CCFMERPLTLT RGSSWAHCSYCHRGATGPWPLTFQVLGTRHLQRRQAQRQGGQR CWSGRCGTWRYRMPCW



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
542	1281	41	1415	TNGRNLLHHWILGVCGMHPHHQETLKKNRVVLAKQLLLSELLE HLLEKDIITLEMRELIQAKVGSFSQNVELLNLLPKRGPQAFDA FCEALRETKQGHLEDMLLTTLSGLQHVLPPLSCDYDLSLPFPV CESCPLYKKLRLSTDTVEHSLDNKDGPVCLQVKPCTPEFYQTH FQLAYRLQSRPRGLALVLSNVHFTGEKELEFRSGGDVDHSTLV TLFKLLGYDVHVLCDQTAQEMQEKLQNFAQLPAHRVTDSCIVA LLSHGVEGAIYGVDGKLLQLQEVFQLFDNANCPSLQNKPKMFF IQACRGGAIGSLGHLLLFTAATASLAL\ETDRGVDQQDGKNHA GSPGCEESDAGKEKLPKMRLPTRSDMICGYACLKGTAAMRNTK RGSWYIEALAQVFSERACDMHVADMLVKVNALIKDREGYAPGT EFHRCKEMSEYCSTLCRHLYLFPGHPPT
543	1282	862	275	VRGKEVMAALCRTRAVAAESHFLRVFLFFRPFRGVGTESGSES GSSNAKEPKTRAGGFASALERHSELLQKVEPLQKGSPKNVESF ASMLRHSPLTQMGPAKDKLVIGRIFHIVENDL\YIDFGGKFHC VCRRPEVDGEKY\QKGTRVR\LRLLDLELTSRFLGATTD\TTV LEANAVLLGIQESKDSRSKEEHLEKYI

ID II NO: N of O Nucleic A	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
544	1283	2	4503	TFGASPAPRRAAPLRLGLRLASGWARAPGGVSPVPGPGMGGDA PTMARAQALVLELTFQLCAPETETPEVGCTFEEGSDPAVPCEY SQAQYDDFQWEQVRLHPGTRAPADLPHGSYLMVNTSQHAPGQR AHVIFQSLSENDTHCVQFSYFLYSRDGHSPGTLGVYVRVNGGP LGSAVWMTGSHGRQWHQAELAVSTFWPNEYQVLFEALISPDR RGYMGLDDILLLSYPCAKAPHFSRLGDVEVNAGQNASFQCMAA GRAAEAERFLLQRQSGALVPAAGVRHISHRRFLATFPLAAVSR AEQDLYRCVSQAPRGRGTSLNFAEFMV/KEPPTPIAPPQLLRA GPTYLIIQLNTNSIIGDGPIVRKEIEYRMARGPWAEVHAVSLQ TYKLWHLDPDTEYEISVLLTRPGDGGTGRPGPPLISRTKCAEP MRAPKGLAFAEIQARQLTLQWEPLGYNVTRCHTYTVSLCYHYT LGSSHNQTI\RECVKTEQGVSRYTMKNLLPYRNVHVRLVLTNP EGRKEGKEVTFQTDEDVPSGIAAESLTFTPLEDMIFLKWEEPQ EPNGLITQYEISYQSIESSDPAVNVPGPRRTISKLRNETYHVF SNLHPGTTYLFSVRARTGKGFGQAALTEITTNISAPSFDYADM PSPLGESENTITVLLRPAQGRGAPISVYQVIVEEEQGSRRLRR EPGGQDCFPVPLTFEAALARGLVDYFGAELAASSLPEAMPFTV GDNKTYRGFWNPPLEPRKAYLIYFQAASHLKGETRLNCIRIAR KAACKESKRPLEVSQRSEEMGLILGICAGGLAVLILLLGAIIV IIRKGRDHYAYSYYPKPVNMTKATVNYRQEKTHMMSAVDRSFT DQSTLQEDERLGLSFMDTHGYSTRGDQRSGGVTEASSLLGGSP RRPCGRKGSPYHTGQLHPAVRVADLLQHINQMKTAEGYGFKQE YESFFEGWDATKKKDKVKGSRQEPMPAYDRHRVKLHPMLGDPN ADYINANYIDIRINREGYHRSNHFIATQGPKPEMVYDFWRMVW QEHCSSIVMITKLVEVGRVKCSRYWPEDSDTYGDIKIMLVKTE TLAEYVVRTFALERRGYSARHEVRQFHFTAWPEHGVPYHATGL LAFIRRVKASTPPDAGPIVHCSAGTGRTGCYIVLDVMLDMAE CEGVVDIYNCVKTLCSRRVMNIQTEEQYIFIHDAILEACLCGE TTIPVSEFKATYKEMIRIDPQSNSSQLREEFQTLNSVTPPLDV EECSIALLPRNRDKNRSMDVLPPDRCLYPFLISTDGDSNNYINA ALTDSYTRSAAFIVTLHPLQSTTPDFWGLVYDYGCTSIVMLNQ LNQSNSAWPCLQYWPEPGRQQYGLMEVBFMSGTADEDLVARVF RVQNISRLQEGHLLVRHFQFLRWSAYRDTPDSKKAFLHLLAEG DKWQAESGDGRTIVHCLNGGGRSGTFCA\CATVLEMIRCHNLV DVFFAAKTLRNYKPNMVETMDQYHFCYDVALEYLEGLESR

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545	1284	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRV SLAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRLGQL SCMSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVAL YKSVPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKE AAVEDLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILN FGQVKNCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSF KNQLVTREGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPG SLMSVNPGMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\ NWGSIRIYFDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMAL RGEHLG/QSFNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALG SL
546	1285	185	3057	AELGLFGSLRFSSLLHFPPRPRSPASACGPGEGRMERGLPLLC AVLALVLAPAGAFRNDKCGDTIKIESPGYLTSPGYPHSYHPSE KCEWLIQAPDPYQRIMINFNPHFDLEDRDCKYDYVEVFDGENE NGHFRGKFCGKIAPPPVVSSGPFLFIKFVSDYETHGAGFSIRY EIFKRGPECSQNYTTPSGVIKSPGFPEKYPNSLECTYI\VFAP KMSEIIL\DFESFDLEPDSNPPGGMFCRYDRLEIWDGFPDVGP HIGRYCGQKTPGRIRSSSGILSMVFYTDSAIAKEGFSANYSVL QSSVSEDFKCMEALGMESGEIHSDQITASSQYSTNWSAERSRL NYPENGWTPGEDSYREWIQVDLGLLRFVTAVGTQGAISKETKK KYYVKTYKIDVSSNGEDWITIKEGNKPVLFQGNTNPTDVVVAV FPKPLITRFVRIKPATWETGISMRFEVYGCKITDYPCSGMLGM VSGLISDSQITSSNQGDRNWMPENIRLVTSRSGWALPPAPHSY INEWLQIDLGEEKIVRGIIIQGGKHRENKVFMRKFKIGYSNNG SDWKMIMDDSKRKAKSFEGNNNYDTPELRTFPALSTRFIRIYP ERATHGGLGLRMELLGCEVEAPTAGPTTPNGNLVDECDDDQAN CHSGTGDDFQLTGGTTVLATEKPTVIDSTIQSEFPTYGFNCEF GWGSHKTFCHWEHDNHVQLKWSVLTSKTGPIQDHTGDGNFIYS QADENQKGKVARLVSPVVYSQNSAHCMTFWYHMSGSHVGTLRV KLRYQKPEEYDQLVWMAIGHQGDHWKEGRVLLHKSLKLYQVIF EGEIGKGNLGGIAVDDISINNHISQEDCAKPADLDKKNPEIKI DETGSTPGYEGEGEGDKNISRKPGNVLKTLEPILITIIAMSAL GVLLGAVCGVVLYCACWHNGMSERNLSALENYNFELVDGVKLK
547	1286	3	521	HEGSALTWASHYQERLNSEQSCLNEWTAMADLESLRPPSAEPG GSVCGGEGLGGGEGRIMQWGAWWRGERAP*LRGSAPRSSEQEQ MEQAIRAELWKVLDVSDLESVTSKEIRQALELRLGLPLQ/PVP *LHRQPDAAAGGTAGPSLPHLPPPLPGLRVERSKPGGAAEEQV GL
548	1287	1742	1200	MAALDLRAELDSLVLQLLGDLEELEGKRTVLNARVEEGWLSLA KARYAMGAKSVGPLQYASHMEPQVCLHASEAQEGLQKFKVVRA GVHAPEEVGPREAGLRRRKGPTKTPEPESSEAPQDPLNWFGIL VPHSLRQAQASFRDGLQLAADIASLQNRIDWGRSQLRGLQEKL KQLEPGAA*

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
549	1288	1	649	HSDVGAATAVLPLLTAVLGVTVVTRRDTEGPGRAALVHLTGSP RQKVGTSGREGLPGLGASCAESELERETQEPRSRGRCIFGAAR WRQVPLASPQRPFLLSPGPRLHRMGLPVSWAPPALWVLGCCAL LLSLWALCTACRRPEDAVAPRKRARRQRARLQGSATAAEAVSA KLSRGPGWGPQGTDQPSSPPVPTEADPPLLPQQVGHQTARAAP G
550	1289	433	632	LTGPGQRLAGTTEGPRRCRGSSQAPTPTWKLVDTRLCAAAPWL ASRAPGHYSQMLLVN*PCRKDWLVSKWMRTPVCGQSPAMTDRP RSEAGRDHRRAKALPGLIPGSNPNLEACGHQALCSSSVASVQG PWPLLPNASSPPTPGQPQP
551	1290	102	612	KHRLCSLEQLMTLISAAREYEIEFIYAISPGLDITFSNPKEVS TLKRKLDQVSQFGCRSFALLFDDIDHNMCAADKEVFSSFAHAQ VSITNEIYQYLGEPETFLFCPT/EYCI*WLYI*LVFLEYITYK GPWAPFSLHFPPPLVCKSRNLFLEDIFQDPKLEKF*ELINDN
552	1291	269	565	TSALTQGLERIPDQLGYLVLSEGAVLASSGDLENDEQAASAIS ELVSTACGFRLHRGMNVPFKRLSVVFGEHTLLVTVSGQRVFVV KRQNRGREPIDV
553	1292	660	233	AKRAERTSRLQGLQHPSPPYPPATLGVTPGQDRTLQLQHQCPA GRKSRKKKSKATQLSPEDRVEDALPPSKAPSRTRRAKRDLPKR TATQRPEGTSLQQDPEAPTVPKKGRRKGRQAASGHCRPRKVKA DIPSLEPEGTSAS
554	1293	590	323	RKSSWLGAVAHACNPSSLGGPGRQITRSGVRDQPGQYGETPSL LKIQTLAGRGGACL*SHILRRLRQKNRLNLGGRGCSELRSRHC APA
555	1294	1	242	AWNSARGAVSPLWVPGCFLTLSVTWIGAAPLILSRIVGGWECE KHSQPWQVLVASRGRAVCGGVLVHPQWVLTAAHCIRK
556	1295	1074	230	AEMADDLGDEWWENQPTGAGSSPEASDGEGEGDTEVMQQETVP VPVPSEKTKQPKECFLIQPKERKENTTKTRKRKKKITDVLAK SEPKPGLPEDLQKLMKDYYSSRRLVIELEELNLPDSCFLKAND LTHSLSSYLKEICPKWVKLRKNHSEKKSVLMLIICSSAVRALE LIRSMTAFRGDGKVIKLFAKHIKVQAQVKLLEKRVVHLGVGTP GRIKELVKQGGLNLSPLKFLVFDWNWRDQKLRRMMDIPEIRKE VFELLEMGVLSLCKSESLKLGLF
557	1296	929	289	RPGTAIWVVECEHGRPIAESEGQEGRGHSPPGPCSVAGFLRGR LGRNLEIMGSTWGSPGWVRLALCLTGLVLSLYALHVKAARARD RDYRALCDVGTAISCSRVFSSRWGRGFGLVEHVLGQDSILNQS NSIFGCIFYTLQLLLGCLRTRWASVLMLLSSLVSLAGSVYLAW ILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRH

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning nucleotide	end nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids		to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
1		to first	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
j .		amino	acid	
		residue	residue	\=possible nucleotide insertion)
		of amino	of amino	
		acid	acid	
			sequence	
558	1297	sequence 2	1063	ESPAPPAFRPAMAAVALMPPPLLLLLLLASPPAASAPSARDPF
336	1291	-	1003	APOLGDTONCOLRCRDRDLGPQPSQAGLEGASESPYDRAVLIS
<u> </u>				ACERGCRLFSICRFVARSSKPNATQTECEAACVEAYVKEAEQQ
			1	ACSHGCWSQPAEPEPEQKRKVLEAPSGALSLLDLFSTLCNDLV
			1	NSAQGFVSSTWTYYLQTDNGKVVVFQTQPIVESLGFQGGRLQR
]		]	]	VEVTWRGSHPEALEVHVDPVGPLDKVRKAKIRVKTSSKAKVES
				EEPODNDFLSCMSRRSGLPRWILACCLFLSVLVMLWLSCSTLV
		<b>!</b>		<del>-</del> -
	i			TAPGQHLKFQPLTLEQHKGFMMEPDWPLYPPPSHACEDSLPPY
				KLKLDLTKL
559	1298	2	485	FPELGTSLSAMRFLAATFLLLALSTAAQAEPVQFKDCGSVDGV
	1			IKEVNVSPCPTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHG
			Į.	ILMGVPVPFPIPEPDGCKSGINCPIQKDKTYSYLNKLPVKSEY
		l		PSIKLVVEWQLQDDKNQSLFCWEIPVQIVSHL
560	1299	1304	919	APETFRCVWRLQGLTFIAFTELQAKVIDTQQKVKLADIQIEQL
	ļ			NRTKKHAHLTDTEIMTLVDETNMYEGVGRMFILQSKEAIHSQL
ļ			<u> </u>	LEKQKIAEEKIKELEQKKSYLERSVKEAEDNIREMLMARRAQ
561	1300	3	799	HSLLLGTRVRDASSKIQGEYTLTLRKGGNNKLSRVFHRDGHYG
			1	FSEPLTFCSVVDLINHYRHESLAQYNAKLDTRLLYPVSKYQQV
İ				RAGLGAREGSTWLAPGLSFLGRPDQAMHLPSFRHVSP\DQIVK
Ì		ł	ļ	EDSVEAVGAQLKVYHQQYQDKSREYDQLYEEYTRTSQELQMKR
			1	TAIEAFNETIKIFEEQGQTQEKCSKEYLERFRREGN/QTKEMQ
			1	RILLNSERLKSRIA\EIHESPHRSWEQQLLVPRASDNKRD/ID
				KPH*TSLKPDL
562	1301	1772	301	AAAAAGRGRSSGRRRRRRPGALFASLGVLLGPRPPPGIPRTRA
				CSMGGVGEPGPREGPAQPGAPLPTFCWEQIRAHDQPGDKWLVI
ł	1			ERRVYDISRWAQRHPGGSRLIGHHGAEDATDAFRAFHQDLNFV
1	1		[	RKFLQPLLIGELAPEEPSQDGPLNAQLVEDFRALHQAAEDMKL
1	-			FDASPTFFAFLLGHILAMEVLAWLLIYLLGPGWVPSALAAFIL
				AISQAQSWCLQHDLGHASIFKKSWWNHVAQKFVMGQLKGFSAH
	]			WWNFRHFOHHAKPNIFHKDPDVTVAPVFLLGESSVEYGKKKRR
	1			YLPYNQQHLYFFLIGPPLLTLVNFEVENLAYMLVCMQWADLLW
			1	AASFYARFFLSYLPFYGVPGVLLFFVAVRVLESHWFVWITQMN
		1		HIPKEIGHEKHRDWVSSQLAATCNVEPSLFTNWFSGHLNFQIE
	1			HHLFPRMPRHNYSRVAPLVKSLCAKHGLSYEVKPFLTALVDIV
1			1	RSLKKSGDIWLDAYLHQ
563	1302	424	93	KSRATRLRESAEMTGFLLPPASRGTRRSCSRSRKRQTRRRRNP
203	1302	744	133	SSFVASCPTLLPFACVPGASPTTLAFPPVVLTGPSTDGIPFAL
ļ	1	]		SLQRVPFVLPSPQVASLPLGHSRG
	1	ļ <u>.                                    </u>	1	IQYRSDLELHSITMKKSGVLFLLGIILLVLIGVQGTPVVRKGR
564	1303	1	414	
	1			CSCISTNQGTIHLQSLKDLKQFAPSPSCEKIEIIATLKNGVQT CLNPDSADVKELIKKWEKQVSQKKKQKNGKKHQKKKVLKVRKS
		1	1	TELNIOUS ADVICED EKKWEKOVSOKKKOKNGKKHOKKKVLKVRKS J
1		ŀ	1	ORSROKKTT

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	corre-	
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
		to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
l	ł	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	ļ	acid	acid	\=possible nucleotide insertion)
ļ	İ	residue of amino	residue of amino	
	1	acid	acid	
	ļ		sequence	'
565	1304	sequence	3007	IPGSTISCRGCCGKWPVOEADPPRAALRGRFPALLTRHCPSPR
1 303	130-	'	3007	AEKEKRSLRRCGCRPLLVELAGPAGQAVEVLPHFESLGKQEKI
				PNKMSAFRNHCPHLDSVGEITKEDLIQKSLGTCQDCKVQGPNL
ļ		ŀ		WACLENRCSYVGCGESQVDHSTIHSQETKHYLTVNLTTLRVWC
1				YACSKEVFLDRKLGTQPSLPHVRQPHQIQENSVQDFKIPSNTT
(	ĺ		1	LKTPLVAVFDDLDIEADEEDELRARGLTGLKNIGNTCYMNAAL
	1	1	1	QALSNCPPLTOFFLDCGGLARTDKKPAICKSYLKLMTELWYKS
		]	1	RPGSVVPTTLFOGIKTVNPTFRGYSQQDAQEFLRCLMDLLHEE
ŀ				LKEOVMEVEEDPOTITTEETMEEDKSQSDVDFQSCESCSNSDR
		Į	<b>'</b>	AENENGSRCFSEDNNETTMLIODDENNSEMSKDWOKEKMCNKI
ĺ		1		NKVNSEGEFDKDRDSISETVDLNNQETVKVQIHSRASEYITDV
ļ			1	HSNDLSTPQILPSNEGVNPRLSASPPKSGNLWPGLAPPHKKAQ
1				SASPKRKKQHKKYRSVISDIFDGTIISSVQCLTCDRVSVTLET
	ļ			FODLSLPIPGKEDLAKLHSSSHPTSIVKAGSCGEAYAPOGWIA
				FFMEYVKRFVVSCVPSWFWGPVVTLQDCLAAFFARDELKGDNM
		ŀ		YSCEKCKKLRNGVKFCKVONFPEILCIHLKRFRHELMFSTKIS
				THVSFPLEGLDLOPFLAKDSPAQIVTYDLLSVICHHGTASSGH
· ·		1	l	YIAYCRNNLNNLWYEFDDQSVTEVSESTVQNAEAYVLFYRKSS
	ł	1	1	EEAOKERRRISNLLNIMEPSLLOFYISROWLNKFKTFAEPGPI
İ		1		SNNDFLCIHGGVPPRKAGYIEDLVLMLPONIWDNLYSRYGGGP
l.		1	1	AVNHLYICHTCQIEAEKIEKRRKTELEIFIRLNRAFQKEDSPA
i		İ	1	TFYCISMOWFREWESFVKGKDGDPPGPIDNTKIAVTKCGNVML
				RQGADSGQISEETWNFLQSIYGGGPEVILRPPVVHVDPDILQA
	ļ		ľ	EEKIEVETRSL
566	1305	28	450	SPSAAGGLAWVSLALGSGSRGRDHSGSGVGTAMAGALVRKAAD
				YVRSKDFRDYLMSTHFWGPVANWGLPIAAINDMKKSPEIISGR
	1			MTFALCCYSLTFMRFAYKVOPRNWLLFACHATNEVAOLIOGGR
				LIKHEMTKTASA
567	1306	133	1292	LGSRQAAGTMRGQRSLLLGPARLCLRLLLLLGYRRRCPPLLRG
			ļ <b>-</b>	LVQRWRYGKVCLRSLLYNSFGGSDTAVDAAFEPVYWLVDNVIR
	'			WFGVVFVVLVIVLTGSIVAIAYLCVLPLILRTYSVPRLCWHFF
1	}	ļ		YSHWNLILIVFHYYOAITTPPGYPPOGRNDIATVSICKKCIYP
	1			KPARTHHCSICNRCVLKMDHHCPWLNNCVGHYNHRYFFSFCFF
			1	MTLGCVYCSYGSWDLFREAYAAIEKMKQLDKNKLQAVANQTYH
				OTPPPTFSFRERMTHKSLVYLWFLCSSVALALGALTVWHAVLI
	1			SRGETSIERHINKKERRRLOAKGRVFRNPYNYGCLDNWKVFLG
	1			VDTGRHWLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV
568	1307	66	962	ATRRRAAEAGMAAVLORVERLSNRVVRVLGCNPGPMTLOGTNT
				YLVGTGPRRILIDTGEPAIPEYISCLKOALTEFNTAIQEIVVT
				HWHRDHSGGIGDICKSINNDTTYCIKKLPRNPOREEIIGNGEQ
			· .	OYVYLKDGDVIKTEGATLRVLYTPGHTDDHMALLLEEENAIFS
	1			GDCILGEGTTVFEDLYDYMNSLKELLKIKADIIYPGHGPVIHN
		ŀ		AEAKIOOYISHRNIREQQILTLFRENFEKSFTVMELVKIIYKN
1				TPENLHEMAKHNLLLHLKKLEKEGKIFSNTDPDKKWKAHL
L	<u> </u>	J	<u> </u>	

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
569	1308	96	1017	ELHRAGQVAGGARRSRRESMELERIVSAALLAFVQTHLPEADL SGLDEVIFSYVLGVLEDLGPSGPSEENFDMEAFTEMMEAYVPG FAHIPRGTIGDMMQKLSGQLSDARNKENLQPQSSGVQGQVPIS PEPLQRPEMLKEETRSSAAAAADTQDEATGAEEELLPGVDVLL EVFPTCSVEQAQWVLAKARGDLEEAVQMLVEGKEEGPAAWEGP NQDLPRRLRGPQKDELKSFILQKYMMVDSAEDQKIHRPMAPKE APKKLIRYIDNQVVSTKGERFKDVRNPEAEEMKATYINLKPAR KYRFH
570	1309	3	526	FITGKGIVAILRCLQFNETLTELRFHNQRHMLGHHAEMEIARL LKANNTLLKMGYHFELPGPRMVVTNLLTRNQDKQRQKRQEEQK QQQLKEQKKLIAMLENGLGLPPGMWELLGGPKPDSRMQEFFQP PPPRPPNPQNVPFSQRSEMMKKPSQAPKYRTDPDSFRVVKLKR IQ
571	1310	3	1858	GGRAGTQCCWRAGARLRGISPSPALPEAPGLCRVRAGLGAGAL GRSPAGRRRGPRVSSSPAPHPRRVLCRCLLFLFFSCHDRRGD SQPYQALKYSSKSHPSSGDHRHEKMRDAGDPSPPNKMLRRSDS PENKYSDSTGHSKAKNVHTHRVRERDGGTSYSPQENSHNHSAL HSSNFTFFLIPSN*PQGKTFRIAPYDS\ADDW/SLEHISSSGE KYYYNCRTEVSQWGKTPKSGLERGQRQKEANKMAVNSFPKDRD YRREVMQATATSGFASGKSTSGDKPVSHSCTTPSTSSASGLNP TSAPPTSASA\VPVSP\VPQ\SPIPPLLQDPNLLRQLL\PALE ATLQLNNSNVDI\SIINEVLTGDVTQASLQTIIHKCLTAGPSV FKITSLISQAAQLSTQAQASNQSPMSLTSDASSPR\SYVSPRN KAHLKLNTVPIQTFGFSTPPVSSQPKVSTPVVKQGPVSQSATQ QPVTADKQQGHEPVSPRSLQRSSSQRSPSPGPNHTSNSSNASN ATVVPQNSSARSTCSLTPALAAHFSENLIKHVQGWPADHAEKQ ASRLREEAHNMGTIHMSEICTELKNLRSLVRVCEIQATLREQR ILFLRQQIKELEKLKNQNSFMV
572	1311	2	1165	VAPECRGAYPFRAMMPGTALKAVLLAVLLVGLQTATGRLLSGQ PVCRGGTQRPCYKVIYFHDTSRRLNFEEAKEACRRDGGQLVSI ESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPY MFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTTPVL PEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLVVTTVV CWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIR KQSEADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPS ESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENEIYGY

,

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first	Predicted end nucleotide location corresponding to first	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino acid residue of amino acid sequence	amino acid residue of amino acid sequence	X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
573	1312	3	1416	TEWGLSGSCPGCSPLEPGSRGRAAAWRILRCRRLPEPSPFLT QPNLAQSQPPAPVPVTDPSVTMHPAVFLSLPDLRCSLLLLVTW VFTPVTTEITSLDTENIDEILNNADVALVNFYADWCRFSQMLH PIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYP TLKLFRNGMMMKREYRGQRSVKALADYIRQQKSDPIQEIRDLA EITTLDRSKRNIIGYFEQKDSDNYRVFERVANILHDDCAFLSA FGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWI QDKCVPLVREITFENGEELTEEGLPFLILFHMKEDTESLEIFQ NEVARQLISEKGTINFLHADCDKFRHPLLHIQKTPADCPVIAI DSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDP TDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL
574	1313	928	142	LTPSVGPVFPGRPTRPLASPFPVPLHRCSAGSQPPGPVPEGLI RIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNKPEWYYTKH PFGHIPVLETSQCQLIYESVIACEYLDDAYPGRKLFPYDPYER ARQKMLLELFCKVPHLTKECLVALRCGRECTNLKAALRQEFSN LEEILEYQNTTFFGGTCISMIDYLLWPWFERLDVYGILDCVSH TPALRLWISAMKWDPTVCALLMDKSIFQGFLNLYFQNNPNAFD FGLC
575	1314	884	363	NTATNMTQPNAGTRKYSVPAISVHTSSSSFAYDREFLRTLPGF LIVAEIVLGLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVF FLIIYITMTYTRIPQVPWTTVGLCFNGSAFVLYLSAAVVDASS VSPERDSHNFNSWAASSFFAFLVTICYAGNTYFSFIAWRSRTI Q
576	1315	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGG SSRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRRR HQRKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYR SRSRSRSRSRGRSYCGRAYALARGQRYYGFGRTVYPEEHSRWR DRSRTRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLP ASLRTVPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQ I

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	
of	of .	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
		to first	to first	T=Threonine, $V=Valine$ , $W=Tryptophan$ , $Y=Tyrosine$ ,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
}		acid	acid	\=possible nucleotide insertion)
ĺ		residue	residue of amino	
1	'	of amino	or amino acid	
	·	acid sequence	sequence	
577	1316	265	2300	AEGSTMDLTKMGMIOLONPNHPTGLLCKANOMRLAGTLCDVVI
] 3,,	1310	203	2300	MVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSPKTFQ
l				OILEYAYTATLOAKAEDLDDLLYAAEILEIEYLEEQCLKMLET
				IQASDDNDTEATMADGGAEEKKDRKARYLKNIFISKHSSEESG
	ļ			YASVAGOSLPGPMVDOSPSVSTSFGLSAMSPTKAAVDSLMTIG
1	Ì	ł		QSLLQGTLQPPAGPEEPTLAGGGRHPGVAEVKTEMMQVDEVPS
		1	1	QDSPGAAESSISGGMGDKVEERGKEGPGTPTRSSVITSARELH
1	1		ļ	YGREESAEOVPPPAEAGOAPTGRPEHPAPPPEKHLGIYSVLPN
		]	Ī	HKADAVLSMPSSVTSGLHVQPALAVSMDFSTYGGLLPQGFIQR
				ELFSKLGELAVGMKSESRTIGEOCSVCGVELPDNEAVEQHRKL
	ļ	}	<b>'</b>	HSGMKTYGCELCGKRFLDSLRLRMHLLAHSAGAKAFVCDQCGA
	}			OFSKEDALETHROTHTGTDMAVFCLLCGKRFOAOSALQOHMEV
	1	ļ		HAGVRSYICSECNRTFPSHTALKRHLRSHTGDHPYECEFCGSC
	ŀ			FRDESTLKSHKRIHTGEKPYECNGCGKKFSLKHQLETHYRVHT
1				GEKPFECKLCHORSRDYSAMIKHLRTHNGASPYOCTICTEYCP
		ĺ		SLSSMOKHMKGHKPEEIPPDWRIEKTYLYLCYV
578	1317	686	908	IWEAPTLIFTLAGGRALGHPPMQKGSQGCALPHPLPGASLPAQ
				PGPADHRGWECRIGGEASVFTHLFCLPHSPT
579	1318	150	1204	ASGSPAPSSSSAMAAACGPGAAGYCLLLGLHLFLLTAGPALGW
1				NDPDRMLLRDVKALTLHYDRYTTSRRLDPIPOLKCVGGTAGCD
	İ			SYTPKVIQCQNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGY
	ĺ	İ		ESSEDQYVLRGSCGLEYNLDYTELGLQKLKESGKQHGFASFSD
1		}	ļ.	YYYKWSSADSCNMSGLITIVVLLGIAFVVYKLFLSDGQYSPPP
		ļ		YSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGF
	1	İ		GSAFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDS
1		ļ		WYYPSYPPSYPGTWNRAYSPLHGGSGSYSVCSNSDTKTRTASG
				YGGTRRR
580	1319	1208	276	GRCGAMAAGLARLLLLIGLSAGGPAPAGAAKMKVVEEPNAFGV
			1	NNPFLPQASRLQAKRDPSPVSGPVHLFRLSGKCFSLVESTYKY
				EFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTGMWMR
1		1	[	DGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFETPL
	1	1		VCHPHALLVYPTLPEALQRQWDQVEQDLADELITPQGHEKLLR
				TLFEDAGYLKTPEENEPTQLEGGPDSLGFETLENCRKAHKELS
	1			KEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLR
	1			GDPGLRGSL
581	1320	1074	132	NSFWSVLFLVQEETEVARCNAQHRLRQSRDSKPDPSFRSQPID
				SSISFAGSDIQPLFSFASVDGTQVGEAEEWAGPWAEATLLPGP
	1		}	GNRWPPRAGLSGNWLEEDGDWPSLPEVVGFVSERELFRDALGA
				GCRILLICEMQLTHQLDLFPECRVTLLLFKDVKNAGDLRRKAM
				EGTIDGSLINPTVIVDPFQILVAANKAVHLYKLGKMKTRTLST
				EIIFNLSPNNNISEALKKFGISANDTSILIVYIEEGEKQINQE
				YLISQVEGHQVSLKNLPEIMNITEVKKIYKLSSQEESIGTLLD
				AIICRMSTKDVL
	1			I

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning mucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
582	1321	5021	7694	QRSWAGPGAGPEAGTRPPARGRRRQPGNVDPRRRAPQLRSQMQ VAMARATTATGNRLWPGLLIMLGSLCHRGSPCGLSTHIEIGHR ALEFLQLHNGRVNYRELLLEHQDAYQAGIVFPDCFYPSICKGG KFHDVSESTHWTPFLNASVHYIRENYPLPWEKDTEKLVAFLFG ITSHMAADVSWHSLGLEQGFLRTMGAIDFHGSYSEAHSAGDFG GDVLSQFEFNFNYLARRWYVPVKDLLGIYEKLYGRKVITENVI VDCSHIQFLEMYGEMLAVSKLYPTYSTKSPFLVEQFQEYFLGG LDDMAFWSTNIYHLTIFMLENGTSDCNLPENPLFIACGGQQNH TQGSKMQKNDFHRNLTTSLTESVDRNINYTERGVFFSVNSWTP DSMSFIYKALERNIRTMFIGGSQLSQKHVSSPLASYFLSFPYA RLGWAMTSADLNQDGHGDLVVGAPGYSRPGHIHIGRVYLIYGN DLGLPPVDLDLDKEAHRILEGFQPSGRFGSALAVLDFNVDGVP DLAVGAPSVGSEQLTYKGAVYVYFGSKQGGMSSSPNITISCQD IYCNLGWTLLAADVNGDSEPDLVIGSPFAPGGGKQKGIVAAFY SGPSLSDKEKLNVEAANWTVRGEEDFSWFGYSLHGVTVDNRTL LLVGSPTWKNASRLGHLLHIRDEKKSLGRVYGYFPPNGQSWFT ISGDKAMGKLGTSLSSGHVLMNGTLKQVLLVGAPTYDDVSKVA FLTVTLHQGGATRMYALTSDAQPLLLSTFSGDRRFSRFGGVLH LSDLDDDGLDEIIMAAPLRIADVTSGLIGGEDGRVYVYNGKET TLGDMTGKCKSWITPCPEEKAQYVLISPEASSRFGSSLITVRS KAKNQVVIAAGRSSLGARLSGALHVYSLGSD
583	1322	1	357	SLRNSARGLKMAASAARGAAALRRSINQPVAFVRRIPWTAASS QLKEHFAQFGHVRRCILPFDKETGFHRGLGWVQFSSEEGLRNA LQQENHIIDGVKVQVHTRRPKLPQTSDDEKKDF
584	1323	1205	433	GSSNIHSASTHGFCHWFSSPSTLKRQKQAIRFQKIRRQMEAPG APPRTLTWEAMEQIRYLHEEFPESWSVPRLAEGFDVSTDVIRR VLKSKFLPTLEQKLKQDQKVLKKAGLAHSLQHLRGSGNTSKLL PAGHSVSGSLLMPGHEASSKDPNHSTALKVIESDTHRTNTPRR RKGRNKEIQDLEESFVPVAAPLGHPRELQKYSSDSESPRGTGS GALPSGQKLEELKAEEPDNFSSKVVQRGREFFDSNGNFLYRI
585	1324	134	954	ETRVKTSLELLRTQLEPTGTVGNTIMTSQPVPNETIIVLPSNV INFSQAEKPEPTNQGQDSLKKHLHAEIKVIGTIQILCGMMVLS LGIILASASFSPNFTQVTSTLLNSAYPFIGPFFFIISGSLSIA TEKRLTKLLVHSSLVGSILSALSALVGFIILSVKQATLNPASL QCELDKNNIPTRSYVSYFYHDSLYTTDCYTAKASLAGTLSLML ICTLLEFCLAVLTAVLRWKQAYSDFPGSVLFLPHSYIGNSGMS SKMTHDCGYEELLTS

			Predicted	A
SEQ	SEQ	Predicted beginning	end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of Nucleic	of Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
1 10.03	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
]		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
	İ	residue	residue	-
	i	of amino	of amino	
		acid	acid	
		sequence	sequence	
586	1325	106	1537	EMVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQP
ł				LFLTPYIEAGKIQKGRELSLVGPFPGLNMKSYAGFLTVNKTYN
		ł	ĺ	SNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGPYV
			İ	VTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVN
i	İ			EDDVARDLYSALIQFFQIFPEYKNNDFYVTGESYAGKYVPAIA
				HLIHSLNPVREVKINLNGIAIGDGYSDPESIIGGYAEFLYQIG
l	İ	i	1	LLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTS
		1	l	DPSYFQNVTGCSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIH
	ļ			VGNQTFNDGTIVEKYLREDTVQSVKPWLTEIMNNYKVLIYNGQ
1		Į	ŀ	LDIIVAAALTERSLMGMDWKGSQEYKKAEKKVWKIFKSDSEVA
	1	}		GYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWD
				PYVG
587	1326	883	541	RDERAKVPFRSTEG\GRRRRRRMEAVVFVFSLLDCCALIFLSV
	i	Į.	ł	YFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTVLLLM
1		ł	į	SLHWFIFLLNLPVATWNIYRYIMVPSGNMGVFDPTEIHNRGQL
1		ł	1 .	KSHMKEAMIKLGFHLLCFFMYLYSMILALIND
588	1327	1126	732	QSPGHGAPCQLSSSHSRSNRLLSPMARATLSAAPSNPRLLRVA
'		1		LLLLLLVAASRRAAGAPLATELRCQCLQTLQGIHLKNIQSVKV
1	1	1	ı	KSPGPHCAQTEVIATLKNGQKACLNPASPMVKKIIEKMLKNGK
		1		SN
589	1328	197	330	HPLSLVFLALNTGKEKSHPGGGGERPGLAGQGEPDHPAGARDG
				R
590	1329	1	1575	CTPVARSMATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTS
		-		TQEYAAKIINTKKLSARDHQKLEREARICRLLKHPNIVRLHDS
	Į	1		ISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQILE
	İ	ļ		SVNHIHOHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQ
1	}	1	1	GEQQAWFGFAGTPGYLSPEVLRKDPYGKPVDIWACGVILYILL
	İ	1		VGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDTVTPEAKNLINQ
				MLTINPAKRITADOALKHPWVCORSTVASMMHROETVECLRKF
1	1			NARRKLKGAILTTMLVSRNFSAAKSLLNKKSDGGVKPQSNNKN
}	}		1	SLVSPAQEPAPLQTAMEPQTTVVHNATDGIKGSTESCNTTTED
1	1			EDLKVRKOEIIKITEQLIEAINNGDFEAYTKICDPGLTSFEPE
				ALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDA
1	1			ACIAYIRLTOYIDGOGRPRTSQSEETRVWHRRDGKWLNVHYHC
			j	SGAPAAPLO
591	1330	17	636	NRRTVKMLLELSEEHKEHLAFLPQVDSAVVAEFGRIAVEFLRR
291	1330	1 "	555	GANPKIYEGAARKLNVSSDTVQHGVEGLTYLLTESSKLMISEL
1		1		DFQDSVFVLGFSEELNKLLLQLYLDNRKEIRTILSEL\APSLP
· ·	1	)		SYHNLEWRLDVQLASRSLRQQIKPAVTIKLHLNQNGDHNTKVL
				OTDPATLLHLVQQLEQALEEMKTNHCRRVVRNIK
F	1 1 2 2 2 4	<del> </del>	237	GTSIYLAHRVA\RAWELAQFIHHTSKKADVVLACGDSIVHPED
592	1331	1	431	LICCPLTGRSCLCDVHLLSSLLARLGRGYAVSLTNL
	1			DICCPDIGROCHCDVILLESSHEARLGRGIAVSEINE

CEO.	CEO	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	beginning	end	
ID NO:	ID NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	согге-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
	110103	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	_
		of amino	of amino	
	Į	acid	acid	
		sequence	sequence	RGCGSCGYKPSAGPAWRPRPPPPAVSPLRHPEPAKVLSFSSCPL
593	1332	2506	1684	
				PALGRTGPSRAARAQSLTMASLFKKKTVDDVIKEQNRELRGTQ
	1			RAIIRDRAALEKQEKQLELEIKKMAKIGNKEACKVLAKQLVHL
·	1			RKQKTRTFAVSSKVTSMSTQTKVMNSQMKMAGAMSTTAKTMQA
		ļ		VNKKMDPQKTLQTMQNFQKENMKMEMTEEMINDTLDDIFDGSD
	1			DEEESQDIVNQVLDEIGIEISGKMAKAPSAARSLPSASTSKAT
		<u> </u>		ISDEEIERQLKALGVD
594	1333	905	432	STDGNGAERLFAELRKMNARGLGSELKDSIPVTELSASGPFES
	ļ	l.		HDLLRKGFSCVKNELLPSHPLELSEKNFQLNQDKMNFSTLRNI
		1		QGLFAPLKLQMEFKAVQQVQRLPFLSSSNLSLDVLRGNDETIG
				FEDILINDPSQSEVMGEPHLMVEYKLGLL
595	1334	111	117	RNMKLHYVAVLTLAILMFLTWLPESLSCNKALCASDVSKCLIQ
				ELCQCRPGEGNCSCCKECMLCLGALWDECCDCVGMCNPRNYSD
	İ	1	l	TPPTSKSTVEELHEPIPSLFRALTEGDTQLNWNIVSFPVAEEL
				SHHENLVSFLETVNQPHHQNVSVPSNNVHAPYSSDK/E*LPTV
				DFFHSAPSCGLSM*SIIFFEET VGGVPTWLEGCGSGNPSPRSGGGPGARLTLPALQMTVHNLYLF
596	1335	817	278	DRNGVCLHYSEWHRKKQAGIPKEEEYKLMYGMLFSIRSFVSKM
			]	; ·
	<u> </u>			SPLDMKDGFLAFQTSRYKLHYYETPTGIKVVMNTDLGVGPIRD VLHHIYSALYVELVVKNPLCPLGQTVQSELFRSRLDSYVRSLP
	l			FFSARAG
507	1226	171	881	PGLSOEPSGSMETVVIVAIGVLATIFLASFAALVLVCRQRYCR
597	1336	1/1	881	PROLLORYDSKPIVOLIGAMETQSEPSELELDDVVITNPHIEA
,	İ	1		ILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKM
ļ.	1			KTSASVSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTAL
}		į.		LLSVSHLVLVTRNACHLTGGLDWIDQSLSAAEEHLEVLREAAL
		1		ASEPDKGLPGPEGFLQEQSAI
<u> </u>	1222	1078	594	ASEPDRGLPGPEGFLQEQSA1   VGMELPAVNLKVILLGHWLLTTWGCIVFSGSYAWANFTILALG
598	1337	10/8	374	VWAVAQRDSIDAISMFLGGLLATIFLDIVHISIFYPRVSLTDT
l	1		1	GRFGVGMAILSLLLKPLSCCFVYHMYRERGGELLVHTGFLGSS
1		1	İ	
F.5.	1335	777	116	QDRSAYQTIDSAEAPADPFAVPEGRSQDARGY PASRPLLGPDTGSVANIFKGLVILPEMSLVIRNLQRVIPIRRA
599	1338	717	116	PLRSKIEIVRRILGVQKFDLGIICVDNKNIQHINRIYRDRNVP
1				TDVLSFPFHEHLKAGEFPQPDFPDDYNLGDIFLGVEYIFHQCK
	1		1	ENEDYNDVLTVTATHGLCHLLGFTHGTEAEWQQMFQKEKAVLD
				ELGRRTGTRLOPLTPGPLPEGAEGRVPF
-	1336	<u> </u>	1004	LRNALDVLHREVPRVLVNLVDFLNPTIMRQVFLGNPDKCPVQQ
600	1339	1	804	
			1	A/MLEPLGSKTETLDLRAEMPITCPTQNEPFLRTPRNSNYTYP
1		1		IKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGD
	1	1		SLTTAVGARPNNSSDLPTSWRGLSWSIGGDGNLETHTTLPNIL
1				KKFNPYLLGFSTSTWEGTAGLNVAAEGARARDMPAQAWDLVER
	1			MKNSPDINLEKDWKLVTLFIGGNDLCHYCENPEAHLATEYVQH
L	L	<u></u>	<u> L.                                    </u>	IQQALDILSE

CEO	CEO	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ ID	SEQ ID	beginning	end	
NO:	NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
of	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
Nucleic	Amino	corre-	corre-	K=Lysine, $L=Leucine$ , $M=Methionine$ , $N=Asparagine$ ,
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
110103	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	•
		of amino	of amino	
		acid	acid	•
		sequence	sequence	
601	1340	1	860	VVEFLWSRRPSGSSDPRPRRPASKCQMMEERANLMHMMKLSIK
1		[	<b>,</b>	VLLQSALSLGRSLDADHAPLQQFFVVMEHÇLKHGLKVKKSFIG
Ì		<u> </u>		QNKSFFGPLELVEKLCPEASDIATSVRNLPELKTAVGRGRAWL
		ĺ	[	YLALMQKKLADYLKVLIDNKHLLSEFYEPEALMMEEEGMVIVG
]			)	LLVGLNVLDANL\CLKGEDLDSQVGVIDFSLYLKDVQDLDGGK
1				EHERITOVLDQKNYVEELNRHLSCTVGDLQTKIDGLEKTNSKL
		1		QERVSAATDRICSLQEEQQQLREQNELIR
602	1341	60	762	KPEGARRVQFVMGLFGKTQEKPPKELVNEWSLKIRKEMRVVDR
[	j			QIRDIQREEEKVKRSVKDAAKKGQKDVCIVLAKEMIRSRKAVS
				KLYASKAHMNSVLMGMKNQLAVLRVAGSLQKSTEVMKAMQSLV
1		l		KIPEIQATMRELSKEMMKAGIIEEMLEDTFESMDDQEEMEEEA
ļ	1			EMEIDRILFEITAGALGKAPSKVTDALPEPEPPGAMAASEDEE
		i		EEEEALEAMQSRLATLRS
603	1342	3	456	RWNSIMELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPI
	ł	<u> </u>		LSYWPYGCHCGLGGRGQPKDATDWCCQTHDCCYDHLKTQGCGI
	İ		· ·	YKDYYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLKRNLD
	ļ	1		TYQKRLRFYWRPHCRGQTPGC
604	1343	249	632	KTVAEEASVGNPEGAFMKMLQARKQHMSTELTIESEAPSDSSG
	}	1		INLSGFGSEQLDTNDESDVSSALSYILPYLSLRNLGAESILLP
				FTEQLFSNVQDGDRLLSILKNNRKSPSQSSLLGNKFKNKIF
605	1344	2	382	LPLTLLLAAPFAHLLLPPGHDQSPCWHPGPALSPGTLGPLSWA
				MANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQL
ļ	İ	1		RSKVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
606	1345	2	987	DPRVRPPLLQPPPPLLPRLVILKMAPLDLDKYVEIARLCKYLP
{		1	1	ENDLKRLCDYVCDLLLEESNVQPVSTPVTVCGDIHGQFYDLCE
				LFRTGGQVPDTNYIFMGDFVDRGYYSLETFTYLLALKAKWPDR
1			1	ITLLRGNHESRQITQVYGFYDECQTKYGNANAWRYCTKVFDML
1	ł			TVAALIDEQILCVHGGLSPDIKTLDQIRTIERNQEIPHKGAFC
ł			1	DLVWSDPEDVDTWAISPRGAGWLFGAKVTNEFVHINNLKLICR
				AHQLVHEGYKFMFDEKLVTVWSAPNYCYRCGNIASIMVFKDVN
Ì				TREPKLFRAVPDSERVIPPRTTTPYFL
607	1346	10	768	SFAGAAARPSTPPASGRGAAPGRPGPSPMDLRAGDSWGMLACL
1	1			CTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLA
				GTYLNYLGPPFNEPDFNPPRLGAETLPRATVDLEVWRSLNDKL
}		}	1	RLTQNYEAYSHLLCYLRGLNRQAATAELRRSLAHFCTSLQGLL
-				GSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWL
1				LKELQTWLWRSAKDFNRLKKKMQPPAAAVTLHLGAHGF
608	1347	114	700	IKISLKKRSMSGISGCPFFLWGLLALLGLALVISLIFNISHYV
				EKORODKMYSYSSDHTRVDEYYIEDTPIYGNLDDMISEPMDEN
				CYEOMKARPEKSVNKMQEATPSAQATNETOMCYASLDHSVKGK
				RRKPRKONTHFSDKDGDEOLHAIDASVSKTTLVDSFSPESQAV
1	1	1		EENIHDDPIRLFGLIRAKREPIN
L	<u> </u>	<u> </u>	<u> </u>	

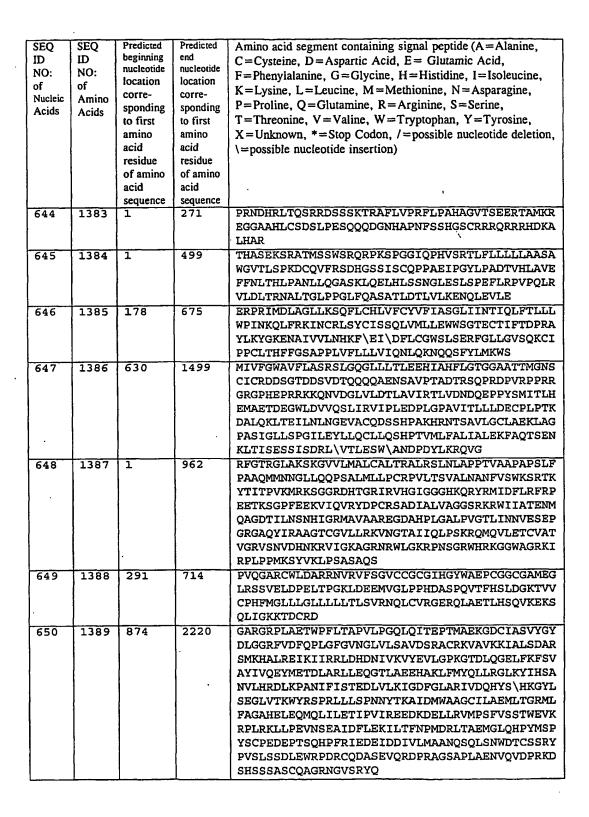
SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
609	1348	2	807	VEFHPQRARAGARAPSMGVLLTQRTLLSLVLALLFPSMASMAA IGSCSKEYRVLLGQLQKQTDLMQDTSRLLDPYIRIQGLDVPKL REHCRERPGAFPSEETLRGLGRRCFLQTLNATLGCVLHRLADL EQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQL LDNSDTAEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYH RFMHSVGRVFSKWGESPNRSRRHSPHQALRKGVRRTRPSRKGK RLMTRGQLPR
610	1349	2	418	DFPGRRFRLVWLLVLRLPWRVPGQLDPTTGRRFSEHKLCADDE CSMLMYRGEALEDFTGPDCRFVNFKKGDPVYVYYKLARGWPEV WAGSVGRTFGYFPKDLIQVVHEYTKEELQVPTNETDFVCFDGG RDDFHNYNV
611	1350	823	115	SPLGKEGGEEVRVKIKDLNEHIVCCLCAGYFVDATTITECLHT FCKSCIVKYLQTSKYCPMCNIKIHETQPLLNLKLDRVMQDIVY KLVPGLQDSEEKRIREFYQSRGLDRVTQPTGEEPALSNLGLPF SSFDHSKAHYYRYDEQLNLCLERLSSGKDKNKSVLQNKYVRCS VRAEVRHLRRVLCHRLMLNPQHVQLLFDNEVLPDHMTMKQIWL SRWFGKPSPLLLQYSVKEKRR
612	1351	9	545	LWWYSAHAAVDAMMDVFGVGFPSKVPWKKMSAEELENQYCPSR WVVRLGAEEALRTYSQIGIEATTRARATRKSLLHVPYGDGEGE KVDIYFPDESSEATTRARATRKSLLHVPYGDGEGEKVDIYFPD ESSEALPFFLFFHGGYWQSGRHPGPHGRPGDPQRCVCPEAVSK QQAFSW
613	1352	49	902	GVRMASRGRRPEHGGPPELFYDETEARKYVRNSRMIDIQTRMA GRALELLYLPENKPCYLLDIGCGTGLSGSYLSDEGHYWVGLDI SPAMLDEAVDREIEGDLLLGDMGQGIPFKPGTFDGCISISAVQ WLCNANKKSENPAKRLYCFFASLFSVLVRGSRAVLQLYPENSE QLELITTQATKAGFSGGMVVDYPNSAKAKKFYLCLFSGPSTFI PEGLSENQDEVEPRESVFTNERFPLRMSRRGMVRKSRAWVLEK KERHRRQGREVRPDTQYTGRKRKPRF
614	1353	1960	871	TLICRMAGCGEIDHSINMLPTNRKANESCSNTAPSLTVPECAI CLQTCVHPVSLPCKHVFCYLCVKGASWLGKRCALCRQEIPEDF LDKPTLLSPEELKAASRGNGEYAWYYEGRNGWWQYDERTSREL EDAFSKGKKNTEMLIAGFLYVADLENMVQYRRNEHGRRRKIKR DIIDIPKKGVAGLRLDCDANTVNLARESSADGADSVSAQSGAS VQPLVSSVRPLTSVDGQLTSPATPSPDASTSLEDSFAHLQLSG DNTAERSHRGEGEEDHESPSSGRVPAPDTSIEETESDASSDSE DVSAVVAQHSLTQQRLLVSNANQTVPDRSDRSGTDRSVAGGGT VSVSVRSRRPDGQCTVTEV

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
615	1354	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWIL GRKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGW GCMLRCGQMIFAQALVCRHLGRDWRWTQRKRQPDSYFSVLNAF IDRKDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVF DTWSSLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDR HCNGFPAGAEVTNRPSPWRPLVLLIPLRLGLTDINEAYVETLK HCFMMPQSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVE PTDGCFIPDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAF GAECCLGMTRKTFGFLRFFFSMLG
616	1355	416	65	PTTSNRAITLTAWPKIPFLGICEAKNPRSENMRLATILEVACH HLGSGPPPSWELWEQGPPGNSSRYIEFLNKHTYIKGTLRVYTK KFCMLVIKSFESKSCVCVYDFDSKSSVNVTV
617	1356	2	382	PRVRFRLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNG SVTSCLELNLYKIAKLQTVNYIALVVGCLLPFFTLSICYLLII RVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPYHT
618	1357	3	672	GRHWLGSAQLTDGGSARKPKMAVPAALILRESPSMKKAVSLIN AIDTGRFPRLLTRILQKLHLKAESSFSEEEEEKLQAAFSLEKQ DLHLVLETISFILEQAVYHNVKPAALQQQLENIHLRQDKAEAF VNTWSSMGQETVEKFRQRILAPCKLETVGWQLNLQMAHSAQAK LKSPQAVLQLGVNNEDSKSLEKVLVEFSHKELFDFYNKLETIQ AQLDSLT
619	1358	557	208	EASSAKTKRKEEKGPKAKMKLMVLVFTIGLTLLLGVQAMPANR LSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDGKGCEMI CYCNFSELLCCPKDVFFGPKISFVIPCNNQ
620	1359	335	1735	KMAEAVFHAPKRKRRVYETYESPLPIPFGQDHGPLKEFKIFRA EMINNNVIVRNAEDIEQLYGKGYFGKGILSRSRPSFTISDPKL VAKWKDMKTNMPIITSKRYQHSVEWAAELMRRQGQDESTVRRI LKDYTKPLEHPPVKRNEEAQVHDKLNSGMVSNMEGTAGGERPS VVNGDSGKSGGVGDPREPLGCLQEGSGCHPTTESFEKSVREDA SPLPHVCCCKQDALILQRGLHHEDGSQHIGLLHPGDRGPDHEY VLVEEAECAMSEREAAPNEELVQRNRLICRRNPYRIFEYLQLS LEEAFFLVYALGCLSIYYEKEPLTIVKLWKAFTVVQPTFRTTY MAYHYFRSKGWVPKVGLKYGTDLLLYRKGPPFYHASYSVIIEL VDDHFEGSLRRPLSWKSLAALSRVSVNVSKELMLCYLIKPSTM TDKEMESPECMKRIKVQEVILSRWVSSRERSDQDDL

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
621	1360	5693	4435	RDIWTMNLQRYWGEIPISSSQTNRSSFDLLPREFRLVEVHDPP LHQPSANKPKPPTMLDIPSEPCSLTIHTIQLIQHNRRLRNLIA TAQAQNQQQTEGVKTEESEPLPSCPGSPPLPDDLLPLDCKNPN APFQIRHSDPESDFYRGKGEPVTELSWHSCRQLLYQAVATILA HAGFDCANESVLETLTDVAHEYCLKFTKLLRFAVDREARLGQT PFPDVMEQVFHEVGIGSVLSLQKFWQHRIKDYHSYMLQISKQL SEEYERIVNPEKATEDAKPVKIKEEPVSDITFPVSEELEADLA SGDQSLPMGVLGAQSERFPSNLEVEASPQASSAEVNASPLWNL AHVKMEPQESEEGNVSGHGVLGSDVFEEPMSGMSEAGIPQSPD DSDSSYGSHSTDSLMGSSPVFNQRCKKRMRKI REQILFIEIRDTAKGGETEQPPSLSPLHGGRMPEMGEGIQSLA
622	1361	15	678	RETQSHRGRRQGWDATWVTRCRESLNRGGAGAGKRAGALAHHV FLALIEPNLAEREASEEEVKACSDETVVADLLVKVVYVLGAIL KIFLREGNVLNQHSGMDIEKYSEHYQHDHSPGAEDDAAGGQLR PTAQERRHKEGSRGSPRCKRARKAVGESPGCPRPRVRPRVRPR VRPRV
623	1362	1080	835	GTRGCCREGTAYAKAYQFMASHLSLGKPVSTGSIPRFNKALFN KQAKCKPNHYSFIGLSMLSPENFSIGCKYSVWFSETKGF
624	1363	872	441	GAQGVRVGIGEVGRVQAPRVSLLHSQGVPRGGTGEAVKEEGRG SSLHPPLPPQGLGEYAACQSHAFMKGVFTFVTGTGMAFGLQMF IQRKFPYPLQWSLLVAVVAGSVVSYGVTRVESEKCNNLWLFLE TGQLPKDRSTDQRS
625	1364	1	585	GTSELLCIQRWNWGPAFPPRPGLALAPTLQLLVEMGSAKSVPV TPARPPPHNKHLARVADPRSPSAGILRTPIQVESSPQPGLPAG EQLEGLKHAQDSDPRSPLGKN*GHGWQVGQGSDLGSPQPLPPS ASHL/YSSRASRCSQPPCLSLPWFGVRSSPANTYHVPVTSLCP SPALHYTALQAGIISTSQARAPR
626	1365	36	381	PLLLPRFIDIPCLLCYLTQVTPDDMYAKAFLIKPNTAITGTDR RKL\RADETTDFP\TLGTDQIYELLPGKDELNIVKSNAHKRDA *TAYVSGENHILSEP*KNLYPAVNTLSSYP
627	1366	763	1003	SRQPPPLLTMVFLLEFLFLVFFPGCVNQLLLSYPWQGQGTSLW SSLSFHWLLPQEDSSRLSIFPLRAGSPPQPAQAPQRI
628	1367	296	1199	KSREQSSLFAADAERSWGGKSCCLLRWRFVGKASHFPRLLPLP GEERPETKERAWKMEQTWTRDYFAEDDGEMVPRTSHTA/ASVS LTAFLSDTKDRGPPVQSQIWRSGEKVPFVQTYSLRAFEKPPQV QTQALRDFEKHLNDLKKENFSLKLLIYFLEERMQQKYEASRED IYKRNTELKVEVESLKRELQDKKQHLDKTWADVENLNSQNEAE LRRQFEERQQEMEHVYELLENKMQLLQEESRLAKNEAARMAAL VEAEKECNLELSEKLKGVTKNWEDVPGDQVKPDQYTEALAQRD K

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  TRRRGTTWRSPRPRRASTSRPSTRPRGVASWPWETAGTATTGP
629	1368	191		GPSARTRRAARRRRSRPRRRAHGGLSQPAGWQSLLSFTILFL AWLAGFSSRLFAVIRFESIIHEFDPWFNYRSTHHLASHGFYEF LNWFDERAWYPLGRIVGGTVYPGLMITAGLIHWILNTLNITVH IRDVCVFLAPTFSGLTSISTFLLTRELWNQGAGLLAACFIAIV PGYISRSVAGSFDNEGIAIFALQFTYYLWVKSVKTGSVFWTMC CCLSYFYMVSAWGGYVFIINLIPLHAFVLVLM/Q/RYSKRVYI *YSTFYIVG
630	1369	852	214	RRLIVVLSDAFLSRAWCSHSF/RVGPARGWVGPSVAPTPLTVP PRREGLCRLLELTRRPIFITFEGQRRDPAHPALRLLRQHRHLV TLLLWRPGSVTPSSDFWKEVQLALPRKVRYRPVEGDPQTQLQD DKDPMLILRGRVPEGRALDSEVDPDPEGDLGVRGPVFGEPSAP PHTSGVSLGESRSSEVDVSDLGSRNYSARTDFYCLVSKDDM
631	1370	246	1091	LSHEGWRRGREGERINSSVASLAPLCILPDLPSNMHLARLVGS CSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALD GINSGITHAGREVEKVFNGLSNMGSHTGKELDKGVQGLNHGMD KVAHEINHGIGQAGKEAEKLGHGVNNAAGQAGKEADKAVQGFH TGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAG KELQNAHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLAS GASVNTPFINLPALWRSVANIMP
632	1371	3150	2792	SASGGLGMTVEGPEGSEREHRPPEKPPRPPRPLHLSDRSFRRK KDSVESHPTWVDDTRIDADAIVEKIVQSQDFTDGSNTEDSNLR LFVSRDGSATLSGIQLATRVSSGVYEPVVIESH
633	1372	667	993	ERSGWPQPEGTVTAQGPLFWERLSGAVTVSSGYKADMWPSFPQ \VRVGSFLFGILFFSFGSSSLPPGLPPPASLLCCAVQWGARAL FLPCLKERALGMEMRNNTLSFRQ
634	1373	636	2	SSSNLRLSFLINENILGKCFRSGPSCAGPRISPLAAQYECPRP SLLIMASVPKTNKIEPRSYSIIPSCGI\RRLGPALNTLIF\QS KRFGPRG\HSAKSIEGAPRGKGRGRAVARLAADRPPAPKIQLR AF*LQQL*YTLLELELPRLLAPDLPSNGSSLKDLKWTHSNYRA SKESCIVIF\VTTSPGREWVICALAAFLGCGS\LSQAPSPES
635	1374	61	519	LRIINTYFCFKFLIVNYIHGTTKARKPHVLGESLISAMSRQEP KMFVLLYVTSFAICASGQPRGNQLKGENYSPRYICSIPGLPGP PGPPGANGSPGPHGRIGLPGRDGRDGRKGEKGEKGTAGLRGKT GPLGLAGEKGDQGETGKKGPIGPE
636	1375	129	579	FASAMLGSRVDRPKLSVAPSVVLEEDQVLVSPAVDLEAGCRLR DFTEKIMNVKGKVILSMLVVSTVIIVFWEFINSTEGSFLWIYH SKNPEVDDSSAQKGWWFLSWFNNGIHNYQQGEEDIDKEKGREE TKGRKMTQQSFGYGTGLIQT

	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide location	nucleotide location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
	of		corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	Amino	corre-		P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding to first	sponding to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
ł			amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
-		amino	acid	
		acid residue	residue	\=possible nucleotide insertion)
		of amino	of amino	1
		acid	acid	
			sequence	
637	1376	sequence	1376	GSHRFSLASPLDPEVGPYCDTPTMRTLFNLLWLALACSPVHTT
637	1376	127	1370	LSKSDAKKAASKTLLEKSQFSDKPVQDRGLVVTDLKAESVVLE
.				HRSYCSAKARDRHFAGDVLGYVTPWNSHGYDVTKVFGSKFTQI
				SPVWLQLKRRGREMFEVTGLHDVDQGWMRAVRKHAKGLHIVPR
				LLFEDWTYDDFRNVLDSEDEIEELSKTVVQVAKNQHFDGFVVE
				VWNQLLSQKRVGLIHMLTHLAEALHQARLLALLVIPPAITPGT
1				
İ		Í		DQLGMFTHKEFEQLAPVLDGFSLMTYDYSTAHQPGPNAPLSWV
		}		RACVQVLDPKSKWRSKILLGLNFYGMDYATSKDAREPVVGARY
				IQTLKDHRPRMVWDSQVSEHFFEYKKSRSGRHVVFYPTLKSLQ
				VRLELARELGVGVSIWELGQGLDYFYDLL
638	1377	998	48	GREGTGWGPAMSEVTRSLLQRWGASFRRGADFDSWGQLVEAID
			]	EYQILARHLQKEAQAQHNNSEFTEEQKKTIGKIATCLELRSAA
		1		LQSTQSQEEFKLEDLKKLEPILKNILTYNKEFPFDVQPVPLRR
				ILAPGEEENLEFEEDEEEGGAGAGSPDSFPARVPGTLLPRLPS
l l		<u> </u>		EPGMTLLTIRIEKIGLKDAGQCINPYITVSVKDLNGIDLTPVQ
1				DTPVASRKEDTYVHFNVDIELQKHVEKLTKGAAIFFEFKHYKP
1. 1		1.	ł	KKRFTSTKCFAFMEMDEIKLGPIVIELYKKPTDFKRKQLQLLT
		ļ		KKPLYLHLHQTLHKE
639	1378	1298	1569	GSITSEPSLDSLQPLPPGFKRFSCLSLPSSWDYRRPPPGLAYF
		1	ŀ	CIFSRDEVSPCWPGCSPSPDLMIRLPRPPSVGITGVSHRAWPT
		}		IDNF
640	1379	196	1197	KMPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRLW
		ł		DSDILCLPGDIVPAPGPVLAPTHLQTELVLRCQKETDCDLCLR
] ]		]	1	VAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLS
1				FQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEV
				RIWSYTQPRYEKELNHTQQLPDCRGLEVWNSIPSCWALPWLNV
		1		SADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWHKNLVRP
			ł	PPSQVHSHCRP\CLCK\DAVPYQRGSLKRTHPKQGKIGGGTSA
				FLVSLTLASSSSSLSSPTSFLYLFHRLDRRSLP
641	1380	756	1110	LRLWNRNQMMHNIIVKELIVTFFLGITVVQMLISVTGLKGVEA
***				QNGSESEVFVGKYETLVFYWPSLLCLAFLLGRFLHMFVKALRV
[ ]				HLGWELQVEEKSVLEVHQGEHVKQLLRIPRP
642	1381	631	1278	KVNRKLRKKGKISHDKRKKSRSKAIGSDTSDIVHIWCPEGMKT
0.32	1201	1031	12,0	SDIKELNIVLPEFEKTHLEHQQRIESKVCKAAIATFYVNVKEQ
] ]			1	FIKMLKESQMLTNLKRKNAKMISDIEKKRQRMIEVQDELLRLE
	l		Ì	PQLKQLQTKYDELKERKSSLRNAAYFLSNLKQLYQDYSDVQAQ
			-	EPNVKETYDSSSLPALLFKARTLLGAESHLRNINHQLEKLLDQ
1	l		[	t e e e e e e e e e e e e e e e e e e e
	L	1	<del> </del>	G
643	1382	1167	755	VWVAMEEPPVREEE*EEGEEDEERDEVGPEGALGKSPFQLTAE
<b>4</b> J	I	1	1	DVYDISYLLGRELMALGSDPRVTQLQFKVVRVLEMLEALVNEG
		1	1 .	AT AT THE IMPORTED DISTRICT PROGRESS CONTINUED CONTINUED
		1		SLALEELKMERDHLRKEVEGLRRQSPPASGEWPDSTKRRPRRK KRKRCCGY



			D-12-12-1	1
SEQ	SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	согте-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
1	Ì	amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
Ì	İ	acid	acid	\=possible nucleotide insertion)
ł		residue	residue	(-possible nucleotide insortion)
į		of amino	of amino	
	1	acid	acid	
1		sequence	sequence	
651	1390	1	2451	MRTLGTCLATLAGLLLTAAGETFSGGCLFDEPYSTCGYSQSEG
332		ļ [—]		DDFNWEQVNTLTKPTSDPWMPSGSFMLVNASGRPEGQRAHLLL
			1	POLKENDTHCIDFHYFVSSKSNSPPGLLNVYVKVNNGPLGNPI
1	]	]	}	WNISGDPTRTWNRAELAISTFWPNFYQVIFEVITSGHQGYLAI
	1		Ĺ	DEVKVLGHPCTRTPHFLRIQNVEVNAGQFATFQCSAIGRTVAG
	İ		1	DRLWLOGIDVRDAPLKEIKVTSSRRFIASFNVVNTTKRDAGKY
1			1	RCMI\RTEGGVGISNYAEL\VVKEPPVPIAPPQLASVGATYLW
			}	IOLNANSINGDGPIVAREVEYCTASGSWNDRQPVDSTSYKIGH
	1	1		LDPDTEYEISVLLTRPGEGGTGSPGPALRTRTKCADPMRGPRK
1	1	ļ	1	LEVVEVKSRQITIRWEPFGYNVTRCHSYNLTVHYCYQVGGQEQ
1			i	
1		i	1	VREEVSWDTENSHPQHTITNLSPYTNVSVKLILMNPEGRKESQ
	1	ł	l	ELIVQTDEDLPGAVPTESIQGSTFEEKIFLQWREPTQTYGVIT
1		Į.	l	LYEITYKAVSSFDPEIDLSNQSGRVSKLGNETHFLFFGLYPGT
	}	1	1	TYSFTIRASTAKGFGPPATNQFTTKISAPSMPAYELETPLNQT
ł				DNTVTVMLKPAHSRGAPVSVYQIVVEEERPRRTKKTTEILKCY
		1	1	PVPIHFQNASLLNSQYYFAAEFPADSLQAAQPFTIGDNKTYNG
1.			1	YWNTPLLPYKSYRIYFQAASRANGETKIDCVQVATKGAATPKP
	1			VPEPEKQTDHTVKIAGVIAGILLFVIIFLGVVLVMKKRLYKHG
1		1	1	ASICSASGEASGSFQSWRKAKHKQACPMARAGARERAGGCLKL
652	1391	30	459	GIRQLLQLSRASMAARKSWTALRLCATVVVLDMVVCKGFVQDL
	İ		1	DESFKENRNDDIWLVHFYAPWCGHCKKLEPIWNEAGLEMKSIG
i	1		ŀ	SPVKAGKMDATSYSSIASEFGVRGYPTIKLALIRPLPSQQMFE
1	1	ì	1	HMHKRHRVFFVYV
653	1392	168	1016	GLVIVISHFSPSPGLLPATQSPAMSDPITLNVGGKLYTTSLAT
	ı		Į.	LTSFPDSMLGAMFSGKMPTKRDSQGNCFIDRDGKVFRYILNFL
1			1	RTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKA
1				EKNAMLNITLNQRVQTVHFTVREAPQIYSLSSSSMEVFNANIF
	1	ŀ		STSCLFLKLLGSKLFYCSNGNLSSITSHLQDPNHLTLDWVANV
	1	1		EGLPEEEYTKQNLKRLWVVPANKQINSFQVFVEEVLKIALSDG
1				FCIDSSHPHALDFMNNKIIRLIRY
654	1393	3	927	SCADNLVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGR
""	-5,5		1	RWAIASDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGG
1				ALLSSYLIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMS
				KLLYIRLALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVV
1				VSWIIIAATVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQL
1				LNGLKTAATSVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTY
				FSDTDLVPSDIAAGLALLHQQQDNIRNNQ\DLPRWSAMPQGAP
1			1	
\	1	<u> </u>	<del> </del>	RKLIWMQN
655	1394	1	716	FRAATAAAKGNGGGGGRAGAGDASGTRKKKGPGPLATAYLVIY
		1		NVVMTAGWLVIAVGLVRAYLAKGSYHSLYYSIEKPLKFFQTGA
		1	1	LLEILHCAIGIVPSSVVLTSFQVMSRVFLIWAVTHSVKEVQSE
				DSVL\FVIAWTITEIIRYSFYTFSLLNHLPYLIKRARYTLFIV
				LYPMGVSGELLTIYAALPFVRQAGLYSISLPNSTKKIFLISQV
	1		1	WWHMLAVSADAKAAEMPAVLKPGP

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A = Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	согге-	corre-	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding	sponding	
		to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
	1	residue	residue	
		of amino	of amino	
		acid	acid	
		sequence	sequence	
656	1395	72	766	MLTGVGCLVSSESLSCVQCNSWEKSCVNSIASECPSHANTSCI
				SSSASSSLETPVRLYQNMFCSAENCSEETHITAFTVHVSAEEH
	ł	1		FHFVSQCCEGKECSNTSDALDPPLKNVSSNAECPACYESNGTS
	ļ	ŀ		CRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATC
	1	1	ļ	QFLSGENKTLGGVIFRKFECANVNSLTPTSAPTTSHNVGSKAS
		1	1	LYLLALASLLLRGLLP
657	1396	97	746	VPARRRAMEIGTEISRKIRSAIKGKLQELGAYVDEELPDYIMV
		] - '		MVANKKSQDQMTEDLSLFLGNNTIRFTVWLHGVLDKLRSVTTE
		1		PSSLKSSDTNIFDSNVPSNKSNFSRGDERRHEAAVPPL\AIPS
		1		ARPEKRDSRVSTSSQESKTTNVRQTYDDGAATRLMSTV/KPLR
	ł	İ	1	EPAPSEDVIDIKPEPDDLIDEDLNFVQEKPLSQKKPTVTLTYG
	Į.	ļ		SSR
	<u> </u>			
658	1397	155	560	ASRVLAAVMGLPWGQPHLGLQMLLLALNWLRPSLSLELVPYTP
	1	ŀ		QITAWDLEGKVTATTFSLEQPRCVFDGLASASDTVWLVVAFSN
				ASRGFQNPETLADIPASPQLLTDGHYMTLPLSPDQLPCGDPMA
		_		GSGSAP
659	1398	416	539	NSLNNFFFETESCCVAQAGVQWRDLGSLQAPPPGFKRFSCL
660	1399	281	736	KSLPLQKHPKPSCQEDQGLGRGSLSGHSPLTLLTFLTSCALGD
ŀ		1	1	QQLLPPRTSGSLCQESMSEQSCQMSELRLLLLGKCRSGKSATG
		1	ļ	NAILGKHVFKSKFSDQTVIKMCQRESWVLRERKVVVIDTPDLF
}	1	}	}	SSIACAEDKQRNIQHLLELSAP
661	1400	2	974	FVETTVSVQSAESSDALSWSRLPRALASVGPEEARSGAPVGGG
	ļ		İ	RWQLSDRVEGGSPTLGLLGGSPSAQPGTGNVEAGIPSGRMLEP
]		ļ	J	LPCWDAAKDLKEPOCPPGDRVGVQPGNSRVWQGTMEKAGLAWT
Ì			ĺ	RGTGVQSEGTWESQRQDSDALPSPELLPQDQDKPFLRKACSPS
				NIPAVIITDMGTQEDGALEETQGSPRGNLPLRKLSSSSASSTG
		-	1	FSSSYEDSEEDISSDPERTLDPNSAFLHTLDQQKPRVVESRSV
1				TQAGVQWHDIGSLQPLPP/WIQAIL/HASAFRIAGTTGACHHA
ł		1	1	RIIFGFLVERGFHHVGQDGLYLLIL
662	1407	222	3	KICSSYFLRIICILQKEAQEASNLYTSCDFFSPAFYFVIYRLY
662	1401	232	3	NFKIHWPGAVAHTYSPSTLGGRGRWVT*GREFM
	1	1050	1	
663	1402	250	556	LILSLPLLYGHLKSYTFPSEHYLHLLQTFATFNKYLNVCVLIF
1	!			IHHKPVVPAIQGTNVGGSLEPRRLRLQQAMIVPLHFGLGNRVR
L_ =	<u> </u>			bcrkkőőőőőőőőkk
664	1403	1	373	RMETKPVITCLKTLLIIYSFVFWITGVILLAAGVWGKLTLGSY
	1	1		ISLIAENSTYAPYVLIVTGTTIVAYPLV*FFFSYSSGFSYILA
	]			VRLIAGIALVYNYIPRSSSRALVRLVVLLRFLLSRHPS
665	1404	3	413	NAEHPGMDRHDLCQKAKLAEHAERDDDMAACMKTVTDQGAELS
	1	-		NEERNLLSDAHTNAV*ARRSSWMGA*RIEQKTEGADTQQQMAP
				DCREIFATELRDICDDVLSLLEKLLIPNASHA*SLVYYLHMIG
1	1			DYYRYWL
1	1.405	<del> </del>	1224	GGGPLGKMPRAQLADPWQMMAVESPSDCADNGQQIMDEPMGED
666	1405	2	334	
1				EISPQTE+VSIKEVAVTHCVKEGHDKADPSQIELLRVLRQGSL
L	<u></u>	<u> </u>	<u></u>	GKVYLGKKVSGSDAKQLYAMKVLT

SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \perpossible nucleotide insertion)
667	1406	2	332	DAAGIRHEAHFGKLECLVQLVRAGA\SLFVSTTRYAQTPA\HI AAFGGHPQCLVWLIQAGANINKPDCEGETPIHKAARSGSLECI SALVANGAHVDNPKKGIRVLEWLFE
668	1407	242	1157	LLKLMFIAELGDYDLAEHSPELVSEFRFVPIQTEEMELAIFEK WKEYRGQTPAQAETNYLNKAKWLEMYGVDMHVVKARDGNDYSL GLTPTGVLVFEGDTKIGLFFWPKITRLDFKKNKLTLVVVEDDD QGKEQEHTFVFRLDHPKACKHLWKCAVEHHAFFRLRGPVQKSS HRSGFIRLGSRFRYSGKTEYQTTKTNKARRSTSFERRPSKRYS RRTLQMKACATKPEELSVHNNVSTQSNGSQQAWGMRSALPVSP SISSAPVPVEIENLPQSPGTDQHDRKWLSAASDCCQRGGNQWN TRAL
669	1408	278	1	ATAPGLFNFF*FLFQCREEHKKKNPEVPVNFAEFSKKCSGRWK TMSSKEKFKFGEMAKADEVCYDREMKDYGPAKGGKKKDPNAPK RPPSGF
670	1409	139	646	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGSKLPSAFCFPG SSVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDL *VLGRPLSYPPWAITTWALPDPFPLSWSPRLTPLGAAQQPLPV LSPVHCLLTSLCRGPDCGVWWMTCQGAQVSIAGALVILWG
671	1410	3	442	LCVSVLCSFSYLQNGWTASDPVHGYWFR\AGDHVSRNIPVATN NPVRAVQEETRDRFHLLGDPQNKDCTLSIRDTRESDAGTYVFC VERGNMKWNYKYDQLSVNVTASQDLLSRYRLEVPESVTVQEGL CVSVP/WQCPLPPLQLDCL
672	1411	84	836	QLQLCQNCTKRGECHCVPFDTYIKTKKEKKRLSVLPPTRLMEA RFSPINQILPWCRQDLAISISKAINTQEAPVKEKHARRIILGT HHEKGAFTFWSYAIGLPLPSSSILSWKFCHVLHKVLRDGHPNV LHDCQRYRSNIREIGDLWGHLHDRYGQLVNVYTKLLLTKISFH LKHPQFPAGLEVTDEVLEKAAGTDVNNM*VTLHGYMASSPRLP HSFLPRLTPRRPHGAVGLNESVALLVDAHAPRDRG
673	1412	307	664	AAPHRMPRAPHFMPLLLLLLLSLPHTQAAFPQDPLPLLISDL QGTSPLSWLPSLEDDAVAA*LGLDFQRFLTLNRTLLVAARDHV FSFDLQAEEEGEGLVPNKYLTWRSQDVENCAVR*KLTLNRTLL VAARDHVFSFDLQAEEEGEGLVPNKYLTWRSQDVENCAVR
674	1413	24	420	HLVPKTRGRGTPSGDQSPVLTLTP*GDPPTILGPQTNQPKEHL TNFKSGKRSFHSLLQPLLLLHPSISPFLNFGSFPFLVETEET CFIHKLKTPALVTPDSLPLVFNHCGDACLIIHPHFRDVEFHHT GN

CEC	CEC	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
SEQ	SEQ	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
ID ID	ID NO:	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Giutainic Acid,
NO:	of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of Nucleic	Amino	corre-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Acids	Amino	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acius	Acias	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	, possible interesting
ļ		of amino	of amino	
ł	]	acid	acid	
		sequence	sequence	
675	1414	1	1101	CCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLK
				PAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTP
1				LAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQL
	Ì	l .		LAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTT
				SATPKPATLL\PTNASVTPSGTSQPQLA\TTAPPVTTVTSQPP
1	ł	1	1	TTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPF
1			1	TEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPG
ļ	j	Ì	ļ	SSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRIL
1	ļ		ì	SESLRRKRYSRLDYLINGIYVDI
676	1415	178	621	IFAGSGVMRLKISLLKEPKHQELVSCVGWTTAEELYSCSDDHH
6/6	1415	1/0	621	IVKWNLLTSETTQIVKLPDDIYPIDFHWFPKSLGVKKQTHAES
l	1	1	]	FVLTSSDGKFHLISKLGRVEKSVEAHCGAVLAGRWNYEGTALV
Ì	1			
<u></u>				TVGEDGQI*IWSKTGMLIS
677	1416	1258	944	ARATTKRHFILLFLFFLRRC\LFLSPRMECNGAILAHCNLHLP
İ				GSSSSASAS*VAGITDVRHHAQLILFVFLVETGFHRVGQAGL
		<u> </u>	<u> </u>	KLLTSGDLLTSASQSAGIIMGISHCAQPKKAF*TKTF
678	1417	876	1291	EAGSNDDLAT*KTCGRARPSSRSRQFGSRVWNHRQGVRSSPGE
	İ	ì	İ	GAGSRSPCRRHRRKHRRNVQSP*RRRSRSCSRRSGRCSVALL
			<b> </b>	GACPVAGHSRGKVVCRRAHAITQRRRCCGFDPMVHPKEHRG*R
Ì	l			ERSRKWSRS
679	1418	262	539	ATAPGLFNFF*FLFQCREEHKKKNPEVPVNFAEFSKKCSGRWK
	İ	l		TMSSKEKFKFGEMAKADEVCYDREMKDYGPAKGGKKKDPNAPK
		ì	1	RPPSGF
680	1419	104	236	LTVNYVLVFSRDSGLRAIENLMQKKGKFDYILLETTGLADPGK
1	1	1	1	K
681	1420	3	277	HEAALCRTRAVAAERHFLRVFLFFRPFRGVGTESGSESGSSKA
				KEPRTPSSSYGTAQYRRWPIAQEYKHCTAHNDTGTLCSELREP
1		}		WRRPQ
682	1421	3	576	EGSSQANTLRSRKENRNNLLACLESHVLR*QFTESHLCSLMGD
				NPFQPKSNSKMAELFMECEEEELEPWQKKVKEVEDDDDDEPIF
				VGEISSSKPAISNILNRVNPSSYSRGLKNGALSRGITAAFKPT
i				SOHYTNPTSNPVPASPINFHPESRSSDSSVIGQPFSKPVSVSK
				TIRPAOGSIGCCLSISTV
683	1422	6	627	CFSLEDILNFFLQGFSAGLFAFYHDKDGNPLTSRFADGLPPFN
003	1422	"		YSLGLYOWSDKVVRKVERLWDVRDNKIVRHTVYLLVTPRVVEE
				ARKHFDCPVLEGMELENQGGVGTELNHWEKRLLENEAMTGSHT
				ONRVLSRITLALMEDTGRQMLSPYCDTLRSNPLQLTCRQDQRA
			1	1 7
<u> </u>				VAV\CNLQKFPKPLPQEYQYFDELSGIPAEDLPYYG

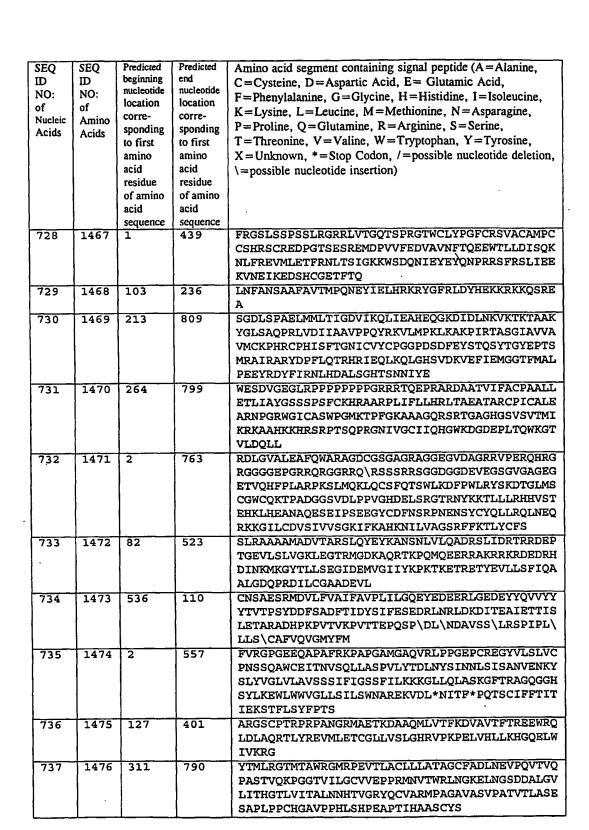
SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
684	1423	1	1272	AARRRQLVSRRRTAE\YPRRRRSSPSARPPDVPGQQPKAAKS PSPVQGKKSPRLLCIEKVTTDKDPKEEKEEEDDSALPQEVSIA ASRPSRGWRSSRTSVSRHRDTENTRSSRSKTGSLQLICKSEPN TDQLDYDVGEEHQSPGGISSEEEEEEEEMLISEEEIPFKDDP RDETYKPHLERETPKPRRKSGKVKEEKEKKEIKVEVEVEVKEE ENEIREDEEPPRKRGRRRKDDKSPRLPKRRKKPPIQYVRCEME GCGTVLAHPRYLQHHIKYQHLLKKKYVCPHPSCGRLFRLQKQL LRHAKHHTDQRDYICEYCARAFKSSHNLAVHRMIHTGEKPLQC EICGFTCRQKASLNWHMKKHDADSFYQFSCNICGKKFEKKDSV VAHKAKSHPEVLIAEALAANAGALITSTDILGTNPES
685	1424	56	526	MTANRIAESLIALSQQEELADLPKDYLLSESEDEGDNDGERKH QKLLEAISSLDGKNRRKLAERSEASLKVSEFNVSSEGSGEKLV LADLLEPVKTSSSLATVKKQLSRVKSKKTVELPLNKEEIERIH REVAFNKTAQVLSKWDPVVLKNRQAEQL*
686	1425	132	344	RIDFMFHSSAMVNSHRKPMFNIHRGFYCLTAILPQICICSQFS VPSSYHFTEDPGAFPVATNGERFPWQELRLPSVVIPLHYDLFV HPNLTSLDFVASEKIEVLVSNATQLIILHSKDLEITNATLQSE EDSRYMKPGKELKVLSYPAHEQIALLVPEKLTPHLKYYVAMDF QAKLGDGFEGFYKSTYRTLGGETRILAVTDFEPTQARMAFPCF DEPLFKANFSIKIRRESRHIALSNMPKVKTIELEGGLLEDHFE TTVKMSTYLVAYI/DL*FPLMGNDFLGRS
687	1426	3	678	RSKIPRSDPRVRTPAPAEAEQGKSQCPSGSTAQSWSAMDILVP LLQLLVLLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNR KMESKKRELFSQIKGLTGASGKVALLELGCGTGANFQFYPPGC RVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLAD GSMDVVVCTLVLCSVQSPRKVLQEVRRVLRPGGVLFFWEHVAE PYGSWAFMW
688	1427	240	641	RLQNSSLMDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALL EKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMM AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSD PTKG
689	1428	1	116	FFFFEMESCSVTQAGVPWHDLSSLQPPPPRFKRFSCLS
690	1429	75	511	DPKAQLPEPLRVLWTAHLVAMAPGSRTSLLLAFALLCLPWLQE AGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQEFEETYIPKDQ KYSFLHDSQTSFCFSDSIPTPSNMEETQQKSNLELLRISLLLI ESWLEPVRILMSIVPN

050	CEC	Dradiesed	Predicted	Amino acid segment containing signal peptide (A=Alanine,			
SEQ	SEQ ID	Predicted beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,			
ID	1	nucleotide	nucleotide	C=Cysteine, D=Aspartic Acid, E= Gidiantic Acid,			
NO: of	NO: of	location	location	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,			
Nucleic	Amino	согте-	corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,			
Acids	Acids	sponding	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,			
110.00	Acids	to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,			
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,			
	]	acid	acid	\=possible nucleotide insertion)			
		residue	residue				
		of amino_	of amino	,			
ĺ '	ĺ	acid	acid	,			
		sequence	sequence	FVKLIKKHOAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLE			
691	1430	2	1364	SQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQ			
ł			ļ	AEEEANLLRRQRQYLELECRRFKRRMLLGRHNLEQDLVREELN			
	ļ	ļ		KROTOKDLEHAMLLROHESMOELEFRHLNTIQKMRCELIRLOH			
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]	1			FQDTCKIQTRQYKALRNHLLETTPKSEHKAVLKRLKEEQTRKL			
)		1	}	AILAEQYDHSINEMLSTQALRLDEAQEAECQVLKMQLQQELEL			
1		[	1	LNAYQSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEEML			
		ĺ	1	ALQNERTERIRSLLERQAREIEAFDSESMRLGFSNMVLSNLSP			
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1	1			POPWGHPS\GPMQ\GVPR/GSSMGVR			
602	1431	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAM			
692	1431	30	304	PLVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYS			
[			•	KIVTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSV			
i	1		ŀ	TSLHSFQVIESLYQKLHEGHGK			
693	1432	130	1671	SSPSRELCFYGFWIASSWWSRWVGSLGPGILPSPPARGRTFAS			
093	1432	1230	1 20 / 2	VSRLPPPWSAGITLTPFLICQSGSVCPGLGAGFGVRSFHHPVA			
		į	Ì	RSAVLLLPLAPAAAQDSTQASTPGSPLSPTEYERFFALLTPTW			
ĺ	{	ĺ	Í	KAETTCRLRATHGCRNPTLVQLDQYENHGLVPDGAVCSNLPYA			
l		ŀ	ŀ	SWFESFCQFTHYRCSNHVYYAKRVLCSQPVSILSPNTLKEIEA			
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		1	1	LSLGGQEQAPEHKQEQGVEHRQEPTQEHKQEEGQKQEEQEEEQ			
				EEEGKQEEGQGTKEGREAVSQLQTDSEPKFHSESLSSNPSSFA			
	1			PRVREVESTPMIMENIQELIRSAQEIDEMNEIYDENSYWRNQN			
	1	<b>\</b>	İ	PGSLLQLPHTEALLVLCYSIVENTCIITPTAKAWKYMEEEILG			
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}	1			SHKTPFVSPLLASQSLSIGNQVGSPESGRFYGLDLYGGLHM			
694	1433	517	578	VSWVPSKDGDVEGARRPFTRLNTSLGPGLQEGRRRTWLVPIPG			
				AVLPGRTQEQPRASPLY*PGAPPCQPQGLVAGPWAQ*AGLRSD			
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				SSAAGDWGSSPRTAQALARPHRLGHHPAAVAPAARLRTQSGHS			
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695	1434	249	632	KTVAEEASVGNPEGAFMKMLQARKQHMSTELTIESEAPSDSSG			
				INLSGFGSEQLDTNDESDVSSALSYILPYLSLRNLGAESILLP			
				FTEQLFSNVQDGDRLLSILKNNRKSPSQSSLLGNKFKNKIF			
696	1435	333	881	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEH			
				VPGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDI			
	1	1	1	TLTVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNI			
1	1		1	FSSPEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGAS			
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SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence 466	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  HEASGVSRALLQSAPGTPATVGISVGELWPFARCCSHSYVRSL
				RGLSVSTHLLCFTIYIMNPSMKQKQEEIKENIKTSSVPRRTLK MIQPSASGSLVGRENELSAGLSKRKHRNDHLTSTTSSPGVIVP ESSENKNLGGVTQESFDLMIKGMKK
698	1437	50	241	PLPARGKSTLPATFCSPSAPELASMSVVPPNRSQTGWPRGVTQ FGNKYIQQTKPLTLERTINL
699	1438	1	422	AEGEDVPPLPTSSGDGWEKDLEEALEAGGCDLETLRNIIQGRP LPADLRAKVWKIALNVAGKGDSLASWDGILDLPEQNTIHKDCL QFIDQLSVPEEKAAELLLDIESVITFYCKSRNIKYSTSLSWIH LLKPLVHLQLP
700	1439	161	413	ALPKFLTHGVKSNERVVVWLFPPSFRAATMVHMNVLPDALKSI NNAERGKPQVLIRLCSKIIIWFLTVMVKYGYIGKFEPTRP
701	1440	211	977	AMAQYGHPSPLGMAAREELYSKVTPRRNRQQRPGTIKHGSALD VLLSMGFPRARAQKALASTGGRSVQAACDWLFSHVGDPFLDDP LPREYVLYLRPTGPLAQKLSDFWQQSKQICGKNKAHNIFPHIT LCQFFMCEDSKVDALGEALQTTVSRWKCKFSAPLPLELYTSSN FIGLFVKEDSAEVLKKFAADFAAEAASKTEVHVEPHKKQLHVT
702	1441	3	408	LAYHFQASHLPTLEKLAQNIDVKLGCDWVATIFSRDIRFA QTRPASPRTARESVLGVSQNMSFNLQSSKKLFIFLGKSLFSLL EAMIFALLPKPRKNVAGEIVLITGAGSGLGRLLALQFARLGSV LVLWDINKEGNEETCKMAREAGATRVHAYTCDCSQKEGVYRVA DQVKK
703	1442	708	244	MVARKGQKSPRFRRVTCFLRLGRSTLLELEPAGRPCSGRTRHR ALHRRLVACVTVSSRRHRKEAGRGRAESFIAVGMAAPSMKERQ VCWGARDEYWKCLDENLEDASQCKKLRSSFESSCPQQWIKYFD KRRDYLKFKEKFEAGQFEPSETTAKS
704	1443	3	475	PAPAARSRELLKELRNGQDMDTVVFEDVVVDFTLEEWALLNPA QRKLYRDVMLETFKHLASVDNEAQLKASGSISQQDTSGEKLSL KQKIEKFTRKNIWASLLGKNWEEHSVKDKHNTKERHLSRNPRV ERPCKSSKGNKRGRTFRKTRNCNRHLRR
705	1444	276	437	CVCGFFVCFETKSCFVAQAGVQWHNLSSLQALPPGFKQFSCLS LLSSWHYRRV
706	1445	2	322	GTRLRRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTYALS SSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGDGE AVGADSGTSSAVSLKNRAAR
707	1446	123	410	DTMQAVVPLNKMTAISPEPQTLASTEQNEVPRVVTSGEQEAIL RGNAADAESFRQRFRWFCYSEVAGPRKALSQLWELCNQWLRPD IHTKE\QILE
708	1447	2	384	PICLFSRPTLRPSRSKVSLIEGRGANMAARWRFWCVSVTMVVA LLIVCDVPSASAQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDK FRRLVKAPPRNYSVIVMFTALQLHRQCVVCKYELQLRFKIK

SEQ ID NO: of Nucleic Acids	SEQ ID NO: . of Amino Acids	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence 535	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  QMRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVS HAISVNHVKRAIAENLWSVCSECLKERRFYDGQLVLTSDIWLC LKCGFQGCGKNSESQHSLKHFKSSRTEPHCIIINLSTWIIWWY
710	1449	116	479	EWDEKIFTPLNKKG  AKERGEERQGEGGGWLSGSRWPLVRSAFVPAPSSLILSMCLSP GIPEAAPDSPLTASAPTP*VMLLGDTGVGKTCFLIQFKDGAFL
711	1450	2	232	SGTFIATVGIDFRVRWLQALASSREPGLWLRHGGV FYPRSSADLPFQTTRCEFQTSVMELAHSLLLNEEALAQITEAK RPVFIFEWLRFLDKVLVAANKVWYCSFFPVALT
712	1451	105	393	MNMKQKSVYQQTKALLCKNFLKKWRMKRESLLEWGLSILLGLC IALFSSSMRNVQFPGMAPQNLGRVDKFNSSSLMVVYTPISNLT QQIMNKTAL
713	1452	2	525	SPQGNGCPDVTGDSVIRVPLTLLVHNLAGLTGLLHHCLSGPLP APSPPPAMSSSRKDHLGASSSEPLPVIIVGNGPSGICLSYLLS GYTPYTKPDAIHPHPLLQRKLTEAPGVSILDQDLDYLSEGLEG RSQSPVALLFDALLRPDTDFGGNMKSVLTWKHRKEHAIPHVVL GR
714	1453	2	1557	NRRTRAQRCQRGRSCGAREEEVEPGTARPPPAASAMDASLEKI ADPTLAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPL QGSGQDMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALL GHSLGAYISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAY FHEEEREGLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSA AARPGLGQYLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEK LIKDDIERGRLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIW LHVEGVNLATLALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVP AVTLYKHDDPALTLVAGLTSNKPTDKLRALPLWLSLQYLGLDG FVERIKHACQLSQRLQESLKKVNYIKILVEDELSSPVVVFRFF QELPGSDPVFKAVPVPNMTPSGVGRERHSCDALNRWLGEQLKQ LVPASGLTVMDLEAEGTCLRFSPLMTAAGKPGLVDIPCFCSGA AG
715	1454	319	873	LCIMDTKEEKKERKQSYFARLKKKKQAKQNAETASAVATRTHT GKEDNNTVVLEPDKCNIAVEEEYMTDEKKKRKSNQLKEIRRTE LKRYYSIDDNQNKTHDKKEKKMVVQKPHGTMEYTAGNQDTLNS IALKFNITPNKLVELNKLFTHTIVPGQVLFVPDANSPSSTLRL SSSSPGATVSPSS
716	1455	60	681	SAGGDSCRAVPMLRFPTCFPSFRVVGEKQLPQEIIFLVWSPKR DLIALANTAGEVLLHRLASFHRVWSFPPNENTGKEVTCLAWRP DGKLLAFALADTKKIVLCDVEKPESLHSFSVEAPVSCMHWMEV TVESSVLTSFYNAEDESNLLLPKLPTLPKNYSNTSKIFSEENS DEIIKLLGDVRLNILVLGGSSGFIELYAYGMFKI
717	1456	357	658	PRDPVTDRARAMPRRGLVAGPDLEYFQRHYFTPAEVAQHNRPE DLWVSYLGRVYDLTSLAQEYKGNLLLKPIVEVAGQDISHWFDP KTRDVSYAGTWDCG

SEQ	SEQ	Predicted	Predicted	Amino acid segment containing signal peptide (A=Alanine,
ID	ID	beginning	end	C=Cysteine, D=Aspartic Acid, E= Glutamic Acid,
NO:	NO:	nucleotide	nucleotide	F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine,
of	of	location	location corre-	K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
Nucleic	Amino	corre-	sponding	P=Proline, Q=Glutamine, R=Arginine, S=Serine,
Acids	Acids	sponding to first	to first	T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine,
		amino	amino	X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
		acid	acid	\=possible nucleotide insertion)
		residue	residue	\=possible nucleotide insertion)
	1	of amino	of amino	
	ļ	acid	acid	
		sequence	sequence	
718	1457	2	481	RIPGRRFRAAFVLGSANVASSVRLRCSFPLSLGGPSGPAAASV
	1	)	ļ	ALGPAGPGRSLGRTPDTGDWEMDSVSFEDVAVAFTQEEWALLD
1	ļ			PSQKNLYRDVMQEIFRNLASVGNKSEDQNIQDDFKNPGRNLSS
	1	ļ		HVVERLFEIKEGSQYGETFSQDSNLNLNKI
719	1458	6	469	SLSLSVSPFLRLSLGRVGGMAEEMESSLEASFSSSGAVSGASG
		-		FLPPARSRIFKIIVIGDSNVGKTCLTYRFCAGRFPDRTEATIG
				VDFRERAVEIDGERIKIQLWDTAGQERFRKSMVQHYYRNVHAV
		ļ	İ	VFVYDMTNMASFHSLPSWIEECKQH
720	1459	82	490	RRPSPGSIVIMAAESDVLHFQFEQQGDVVLQKMNLLRQQNLFC
/		1		DVSIYINDTEFQGHKVILAACSTFMRDQFLLTQSKHVRITILQ
	İ	1	ì	SAEVGRKLLLSCYTGALEVKRKELLKYLTAASYLQMVHIAEKR
	ļ		ł	TEAFVKF
721	1460	48	708	AEGLOSAAGIRIDTKAGPPEMLKPLWKAAVAPTWPCSMPPRRP
'			1	WDRQAGTLQVLGALAVLWLGSVALICLLWQVPRPPTWGQVQPK
ļ		ļ	1	DVPRSWEHGSSPAWEPLEAEARQQRDSCQLVLVESIPQDLPSA
	•		ĺ	AGSPSAOPLGOAWLOLLDTAQESVHVASYYWSLTGPDIGVNDS
1	ł	1		SSOLGEALLOKLOOLLGRNISLAVATSSPTLARTSTDLQVLAA
'		į		RGAH
722	1461	436	677	RKKKMPLPFGLKLKRTRRYTVSSKSCLVARIQLLNNEFVEFTL
		}		SVESTGQESLEAVAQRLELREVTYFSLWYYNKQNQRR
723	1462	45	569	LQPLSSWESASEVTRSPVSPEDVKQATSNFENLQKQLARKMKL
'		1	1	PIFIADAFTARAFRGNPAAVCLLENELDEDMHQKIAREMNLSE
	1		i	TAFIRKLHPTDNFAQSSCFGLRWFTPASEVPLCGHATLASAAV
	ļ	1	İ	LFHKIKNMNSTLTFVTLSGELRARRAEDGIVLDLPLYPAHPQD
	}	1	1	FHE*
724	1463	79	530	AADTMQSDDVIWDTLGNKQFCSFKIRTKTQSFCRNEYSLTGLC
1	- 333	1		NRSSCPLANSQYATIKEEKGQCYLYMKVIERAAFPRRLWERVR
i				LSKNYEKALEOIDENLIYWPRFIRHKCKQRFTKITQYLIRIRK
	1		i	LTLKRORKLVPLSKKVERREK
725	1464	2	261	FVERGLGDPALPTLMFEEPEWAEAAPVAAGLGPVISRPPPAAS
				SQNKVSDSREQWELFQAAKRTLVDPSAVCIAGRDTCGTVKGES
726	1465	1	860	VVEFLWSRRPSGSSDPRPRRPASKCOMMEERANLMHMMKLSIK
		-		VLLQSALSLGRSLDADHAPLQQFFVVMEHCLKHGLKVKKSFIG
1				QNKSFFGPLELVEKLCPEASDIATSVRNLPELKTAVGRGRAWL
	1			YLALMQKKLADYLKVLIDNKHLLSEFYEPEALMMEEEGMVIVG
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1	]		1	QERVSAATDRICSLQEEQQQLREQNELIR
727	1466	69	452	GCYAPSPHLGGSLTPRFFPNGVFHRRLPRPRPPQPPSVSSAPT
'='	1.400		132	LRPLCAHFSLGKLRLRVRKSAEVAPPRTEKGWGSAEPRHSRAP
				LGLQGLRMAASAQVSVTFEDVAVTFTQEEWGQLDAAQRTLY
	<u> </u>	<u> </u>		PARAGEMENTA LI ED AVAIL I ARRINGARANGELLI



SEQ ID NO: of Nucleic Acids	SEQ ID NO: of Amino Acids	Predicted beginning nucleotide location corre- sponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)  WGRROLVSEAARAOGDPVCSTMSEEEAAQIPRSSVWEQDQQN
738	1477	2	421	VVQRVVALPLVRATCTAVCDVYSAAKDRHPLLGSACRLAENCV CGLTTRALDHAQPLLEHLQPQLATMNSLACRGLDKLEEKLPFL QQPSETVVTS
739	1478	256	1250	AKAFTMAESPGCCSVWARCLHCLYSCHWRKCPRERMQTSKCDC IWFGLLFLTFLLSLSWLYIGLVLLNDLHNFNEFLFRRWGHWMD WSLAFLLVISLLGTYASLLLVLALLLRLCRQPLHLHSLHKVLL LLIMLLVAAGLVGLDIQWQQERHSLRVSL/QDCR*L*TPAVRP *EESGEGHWRRAHLTSSCPQATAPFLHIGAAAGIALLAWPVAD TFYRIHRREPKILLLLLFFGVVLVIYLAPLCISSPCIMEPRDL PPKPGLVGHRGAPMLAPENTLMSLRKTAECGATVFETDVMVSS DGVPFLMHDEHLSRTTNVASVFPTRITAHSS

# WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-739, a mature protein coding portion of SEQ ID NO:1-739, an active domain of SEQ ID NO: 1-739, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:



- (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-739.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

 a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-739, a mature protein coding portion of SEQ ID NO: 1-739, an active domain of SEQ ID NO: 1-739, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-739, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).



- 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 740-1478, the mature protein portion thereof, or the active domain thereof.
- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-739.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computerreadable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

#### SEQUENCE LISTING

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gacccacagt	ggatggagac	cattggcagg	gacctgcacc	gtcaattccc	tctgcacgag	660
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<210> 5 <211> 536 <212> DNA <213> Homo sapiens

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<210> 6 <211> 780 <212> DNA <213> Homo sapiens

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<210> 7
<211> 654
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
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<223> n = a,t,c or g
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	tgcacacaga					180
	attctgatct					240
	gtcctgaccc					300
tgactatcag	gccatgtgca	aaccctcgag	tcaccaccac	agtgcagccc	agcccctggt	360
cagcccaatt	tctgccttct	tgacggcgac	caggtggctg	ctgcaggagc	tggtgctgtt	420
	tggagtgtct					480
tcttccatca	ctcccacaaa	cacaagaagc	aggacccgct	gcagccctgc	gacacggagt	540
	cgtgtaccag					600
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<210> 8
<211> 469
<212> DNA
<213> Homo sapiens
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                                                                    120
                                                                    180
gcctggcgca agcgctggtt tgtcctccgg cgaggccgca tgagcggcaa ccccgatgtc
                                                                    240
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tgtgcagtgt ggaagcatgt gggccccagc tttgttcgga aggaatttca gaataatttc
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                                                                    360
atgcaggtgt gggtgcacag catcagtcag gtctgcaacc ttggccacct ggaggatggt
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                                                                    469
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<210> 9
<211> 409
<212> DNA
<213> Homo sapiens
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<220>

# WO 01/53455

<221> misc_feature <222> (1)...(409) <223> n = a,t,c or g

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<210> 10 <211> 1145 <212> DNA <213> Homo sapiens

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		gttccgaata				180
ctgggacagt	gtcttctcag	aaacaaccag	ccttgaaggc	tacaagtgac	aagaaagatt	240
		gaaataaagg				300
		gctacaagtg				360
cagaaataaa	ggatggacaa	ataccgtggg	acagtgtctt	ctcagagaca	accagccttg	420
aaggcttaca	ggtgatgaga	aagattctgt.	ttcgaatata	gccagagaaa	taaaggatgg	480
agaaaaatct	gggacagtgt	ctcctcagaa	acaatcggcc	cagaaggtta	tatttaaaaa	540
		ttgccacaag				600
gtatcctgag	aatctgccca	ccttgaaggc	tacaattgaa	aataaaaatt	ctgttctgaa	660
		atgtacaaac				720
		ggcttgaaga				780
		accttgatga				840
		gtaattgtaa				900
		ttcacctatt				960
		ataatcactg				1020
		tacaaaagag				1080
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gcaag	-		_			1145

<210> 11

<211> 890

<212> DNA

<213> Homo sapiens



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gagtcgtctt	taatgagatg	aagggagcgt	ttacagacaa	tgagaggata	ttctcccagc	720
accttcagaa	cagacttctt	cctgaccaca	cgtactcagt	ggtctccggg	ggtgacccac	780
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<210> 12
<211> 982
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
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<223> n = a,t,c or g
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<210> 13 <211> 440 <212> DNA <213> Homo sapiens

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gccagtcttt	tggtaagaac	tagtcacaca	gacctcaacc	tgatgcgtgg	agacaaggaa	180
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<210> 14 <211> 581 <212> DNA

<213> Homo sapiens

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693

<210> 16 <211> 562 <212> DNA <213> Homo sapiens

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<210> 18 <211> 519

<212> DNA

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#### <213> Homo sapiens

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ccagggagcg	tgttcgagct	gtgtacaaag	aggcccagta	ctatgccatc	gggcccctcc	480
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<210> 19 <211> 460 .

<212> DNA

<213> Homo sapiens

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<210> 20 <211> 731 <212> DNA <213> Homo sapiens

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<211> 556

<212> DNA

<213> Homo sapiens

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<211> 422

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<213> Homo sapiens

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<210> 27 <211> 850 <212> DNA <213> Homo sapiens

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<210> 28 <211> 990 <212> DNA <213> Homo sapiens

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	actcctaact					420
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	aggcagttct					660
	tggaaggete					720
	ccccggaccc					780
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<210> 29 <211> 622 <212> DNA <213> Homo sapiens

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<210> 31 <211> 1956 <212> DNA

<213> Homo sapiens

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#### <213> Homo sapiens

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<213> Homo sapiens

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<211> 600

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<210> 37 <211> 429 <212> DNA

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555

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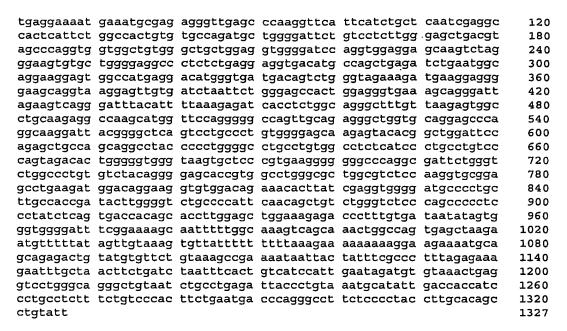
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<211> 481

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<213> Homo sapiens

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<213> Homo sapiens

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<210> 59 <211> 711 <212> DNA <213> Homo sapiens

<400> 59 60 ggaaaatagc agattttggg ttcagtaacc tcttcactcc tgggcagctg ctgaagacct 120 ggtgtggcag ccctccctat gctgcacctg aactetttga aggaaaagaa tatgatgggc 180 ccaaagtgga catctggagc cttggagttg tcctctacgt gcttgtgtgc ggtgccctgc 240 catttgatgg aagcacactg cagaatctgc gggcccgcgt gctgagtgga aagttccgca 300 teceattttt tatgteeaca gaatgtgage atttgateeg ceatatgttg gtgttagate 360 ccaataagcg cctctccatg gagcagatct gcaagcacaa gtggatgaag ctaggggacg 420 ccgatcccaa ctttgacagg ttaatagctg aatgccaaca actaaaggaa gaaagacagg tggaccccct gaatgaggat gtcctcttgg ccatggagga catgggactg gacaaagaac 480 agacactgca gtcattaaga tcagatgcct atgatcacta tagtgcaatc tacagcctgc 540 600 tgtgtgatcg acataagaga cataaaaccc tgcgtctcgg agcacttcct agcatgcccc

gagccctggg cctttcaagc accagtcaat atccaggcgg agcaggcagg tactgctatg 660 aacatcagcg ttccccaggt gcagctgatc aacccagaga accaaattgt g 711

<210> 60 <211> 344 <212> DNA <213> Homo sapiens

<400> 60
ggcacgagaa tttttaggcc accgagcttc tataacatgg tcatgagctc gggtgcacca 60
tagatttccc aaagctgagg ttgcataacc cctctgctga ggacagatct taccgaagat 120
cgcacgaagt gctgccatgg agatctgctt gaatgcgctg atgacagggc agaccttgtc 180
gaggatatct gggaaaatca agattcaatc tccactatac tgattgaatg ctgtgaaaaa 240
cctctgttgg aaaaatccca ctgcattgcc gaagtggaaa atgatgagat gcctgctgac 300
ttgccttcat tagctgctga ttttgttgaa agtaaggatg tttg

<210> 61 <211> 594 <212> DNA <213> Homo sapiens

<400> 61 gettgagete gagegaegge getggeggag aegeeggetg etecteeeet ceeegeeget 60 tttcctaaaa ggattgtaca ccttagaagt gcttaaggaa gagtgatgaa gctctgaatc 120 180 gtgtcctgca gcagattctg agtgccaccc aagatgaaga gagggacaag cttgcatagt 240 aggeggggea agecagagge cecaaaggga agtececaaa teaacaggaa gtetggteag 300 gagatgacag ctgttatgca gtcaggccga cccaggtctt catccacaac tgatgcacct accegatety ctatgatgga aatagettyt getgetgety etgetgetge tyeatyteta 360 ccaggagagg agggaactgc ggagcggatc gaacggttgg aagtaagcag ccttgcccaa 420 acatecagtg cagtggcete cagtacegat ggcagcatec acacagacte tgtggatgga 480 acaccagacc ctcagcgcac aaaggctgcc attgctcacc tgcagcagaa gatcctgaag 540 ctcacagaac aaatcaagat tgcacaaaca gcccgacgaa atcgtcgacc cggg 594

<210> 62 <211> 1609 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (1)...(1609) <223> n = a,t,c or g

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                                                                      60
ttcgaaggat cgctttaqct gaatatcaga gaaccttgtg aagatcttaa agagcaacta
                                                                      120
aagcataaag aatttettet ggetgetaat acttgtaace gtgttggtgg tetttgtttg
                                                                      180
                                                                      240
aaatgtgetc agcatgaagc tgttetttec caaacccata ctaatgttca tatgcagacc
                                                                      300
atcgaaagac tggttaaaga aagagatgac ttgatgtctg cactagtttc cgtaaggagc
                                                                      360
agettggeag atacgeagea aagagaagea agtgettatg aacaggtgaa acaagttttg
caaatatctg aggaagccaa ttttgaaaaa accaaggctt taatccagtg tgaccagttg
                                                                      420
                                                                      480
aggaaggagc tggagaggca ggcggagcga cttgaaaaag aacttgcatc tcagcaagag
                                                                      540
aaaagggcca ttgagaaaga catgatgaaa aaggaaataa cgaaagaaag ggagtacatg
                                                                     600
ggatcaaaga tgttgatctt gtctcagaat attgcccaac tggaggccca ggtggaaaag
                                                                     660
gttacaaagg aaaagatttc agctattaat caactggagg aaattcagag ccagctggct
tctcgggaaa tggatgtcac aaaggtgtgt ggagaaatgc gctatcagct gaataaaacc
                                                                      720
aacatggaga aggatgaggc agaaaaggag cacagagagt tcagagcaaa aactaacagg
                                                                     780
gatcttgaaa ttaaagatca ggaaatagag aaattgagaa tagaactgga tgaaagcaaa
                                                                      840
                                                                    . 900
caacacttgg aacaggagca gcagaaggca gccctggcca gagaggagtg cctgagacta
acagaactgc tgggcgaatc tgagcaccaa ctgcacctca ccagacagga aaaagatagc
                                                                     960
attcagcaga gctttagcaa ggaagcaaag gcccaagccc ttcaggccca gcaaagagag
                                                                    1020
caggagetga cacagaagat acagcaaatg gaggeecage atgacaaaac tgaaaatgaa
                                                                    1080
cagtatttgt tgctgacctc ccagaataca tttttgacaa agttaaagga agaatgctgt
                                                                    1140
                                                                    1200
acattageca agaaactgga acaaatetet caaaaaaeca gatetgaaat ageteaaete
agtcaagaaa aaaggtatac atatgataaa ttgggaaagt tacagagaag aaatgaagaa
                                                                    1260
ttggaggaac agtgtgtcca gcatgggagg agtacatgag acgatgaagc aaaggctaag
                                                                    1320
gcaggtggat aagcacaggc aggccacagc ccaggaggtg gtgcaggtcc ccagaagcag
                                                                    1380
gacengette tteenggaga gggagggnet gteggaagag gtgggneegn ettggggnee
                                                                    1440
nngttaccca gnatncncaa tctttttgg ttgacccggt tggacagggt ggacttnant
                                                                    1500
gttttncaaa ggngnttttt cattccanct tgttttngct taatttngcn caacgnaccc
                                                                    1560
acggcctncc cggnntgaaa ccccccnccc tgagggggg ttntccccc
                                                                    1609
```

```
<210> 63
<211> 615
<212> DNA
```

<213> Homo sapiens

```
<400> 63
catcctatcc cgtgtggtgg aattcgccgc tgactgctga ggtgccaccc gagctgctgg
                                                                       60
etgetgeegg ettetteeae acaggeeate aggacaaggt gaggtgette ttetgetatg
                                                                      120
                                                                      180
ggggcctgca gagctggaag cgcggggacg acccctggac ggagcatgcc aagtggttcc
                                                                      240
ccagctgtca gttcctgctc cggtcaaaag gaagagactt tgtccacagt gtgcaggaga
                                                                      300
eteactecca getgetggge tettgggace egtgggaaga aceggaagae geageceetg
                                                                      360
tggccccctc cgtccctgcc tctgggtacc ctgagctgcc cacacccagg agagaggtcc
                                                                      420
agtetgaaag tgeecaggag ceaggagggg teagteeage egaggeecag agggegtggt
                                                                      480
gggttcttga gcccccagga gccagggatg tggaggcgca gctgcggcgg ctgcaggagg
                                                                      540
agaggacgtg caaggtgtgc ctggaccgcg ccgtgtccat cgtctttgtg ccgtgcgcc
                                                                      600
acetggtetg tggetgagtg tgeeceegge etgeagetgt geeceatetg geagaageee
                                                                      615
ccgtcccgca gccgg
```

<210> 64 <211> 839

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<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1) ... (839)
<223> n = a,t,c or g

<400> 64 aagaatgtet ggaagagatg gaagaaaagg ttttttgtat tggtgcaggt cattcagtac 60 acgtttgcca tgtgcagtta tcgggagaag aaagcggagc ctcaggaact tctacaattg 120 gatggctaca ctgtggatta caccgacccc cagccaggtt tggagggtgg ccgagccttc 180 ttcaatgctg tcaaggaggg agacaccgtg atatttgcca gtgacgatga acaagaccgc 240 atcctgtggg tccaggccat gtatcgggcc acggggcagt cacacaagcc tgtgccccg 300 acccaagtcc agaaactcaa cgccaaggga ggaaatgtac ctcagctgga tgcccctatc 360 teteaatttt aegeagatag ageteaaaaa catggeatgg atgaatttat etetteeaae 420 ccctgtaact ttgaccacgc ttccctcttt gagatggtac aacgccttac tttggatcac 480 agacttaatg attectatte ttgcctggge tggtteagte etggccaggt gtttgtacta 540 gacgagtatt gcgcccgaaa tqgagtccgg gggtgtcacc gacatctctg ctacctcaga 600 gacttgcttg aacgggcaga aaatggcgcc atgatcgacc ccacccttnt tcactacagc 660 tttgecttet gtgeateeea tgteeatggg aacaggeetg atggaattgg gaactgttga 720 ctgttgaaga aaaggaacgt tttttgaagg aaatcaaaag aggaggnttc cgnagttctg 780 ctaagaaaaa tcaggttaca acattttagg naattgcttt tcccatttgg gtcgaacct 839

<210> 65 <211> 1678 <212> DNA <213> Homo sapiens

<400> 65 caagcagetg atcgtgctgg gaaacaaagt ggacctcctg ccccaggatg ctcctggcta 60 ceggeagagg ctgegggage gactgtggga ggactgtgee egegeeggge teetgetgge 120 ccctggccac caagggccac agcgcccgt caaggacgag ccacaggacg gggagaatcc 180 gaateegeeg aactggteee geacagtggt cagggaegtg eggetgatea gegecaagae 240 cggctatgga gtggaagagt tgatctctgc ccttcagcgc tcctggcgct accgtgggga 300 cgtctactta gtgggcgcca ccaacgccgg caaatccact ctctttaaca cgctcctgga 360 gtccgattac tgcactgcca agggetccga ggccatcgac agagccacca tctccccttg 420 gccaggtact acattaaacc ttctgaagtt tcctatttgc aacccaactc cttacagaat 480 gtttaaaagg catcaaagac ttaaaaaaga ttcaactcaa gctgaagaag atcttagtga 540 gcaagaacaa aatcagctta atgtcctcaa aaagcatggt tatgtcgtag gaagagttgg 600 aaggacatto ttgtattcag aagaacagaa ggataacatt cootttgagt ttgatgotga 660 ttcacttgcc tttgacatgg aaaatgaccc tgttatgggt acacacaaat ccaccaaaca 720 agtagaattg actgcacaag atgtgaaaga tgcccactgg ttttatgaca cccctggaat 780 tacaaaagaa aattgtattt taaatcttct aacagaaaaa gaagtaaata ttgttttgcc 840 aacacagtcc attgttccaa gaacttttgt gcttaaacca ggaatggttc tgtttttggg 900 tgctataggc cgcatagatt tcctgcaggg aaatcagtca gcttggttta cagtcgtggc 960 ttccaacatc ctccctgtgc atatcacctc cttggacagg gcagacgctc tgtatcagaa 1020 gcatgcaggt catacgttac tccagattcc aatgggtgga aaagaacgaa tggcaggatt 1080 tectectett gttgetgaag acattatgtt aaaagaagga etgggggeat etgaageagt 1140 ggccgacatc aagtttteet etgcaggttg ggttteagta acacctaatt ttaaggacag 1200 actgcatctc cgaggctata cacctgaagg aacagttttg accgtccggc cccctctctt 1260 gccatatatt gttaacatca aaggacagcg catcaagaaa agtgtggcct ataaaaccaa 1320

gaagcctcct	tcccttatgt	acaacgtgag	gaagaagaaa	ggaaagataa	atgtatgaga	1380
ccgaccttgt	tcactccaga	tattaactgt	attgaacaca	acaaaataca	ttgaatttgt	1440
attaaacata	taacgcataa	ataaagctcc	cattcttacc	cttaaaaata	aaaggagaat	1500
gaaaaaaaaa	gatgccaata	ggcatatacg	tggttttggg	tattccgggg	tcttcccgtg	1560
gtctgttcac	tttgcggtgg	tggtgatata	ttaggcagtc	ggggcgcctg	atgtacgcct	1620
tcttatagag	gtacatggtt	ggatgcagcg	tcttgacgtg	ggattcgctt	tattcgcc	1678

<210> 66 <211> 1888 <212> DNA <213> Homo sapiens

<400> 66 tccacggtgg catccatgat gcatcgtcag gagactgtgg agtgtttgcg caagttcaat 60 gcccggagaa aactgaaggg tgccatcctc acgaccatgc ttgtctccag gaacttctca 120 gctgccaaaa gcctattgaa caagaagtcg gatggcggtg tcaagccaca gagcaacaac 180 240 aaaaacagte tegtaageee ageecaagag eeegegeeet tgeagaegge catggageea caaaccactg tggtacacaa cgctacagat gggatcaagg gctccacaga gagctgcaac 300 accaccacag aagatgagga ceteaaaget geeeegetee geaetgggaa tggeageteg 360 gtgcctgaag gacggagete ccgggacaga acageceeet etgcaggeat geageeeeag 420 cettetetet geteeteage catgegaaaa caggagatea ttaagattae agaacagetg 480 attgaagcca tcaacaatgg ggactttgag gcctacacga agatttgtga tccaggcctc 540 acttectttg ageetgagge cettggtaac etegtggagg ggatggattt ceataagttt 600 tactttgaga atctcctgtc caagaacagc aagcctatcc ataccaccat cctaaaccca 660 720 cacgtccacg tgattgggga ggacgcagcg tgcatcgcct acatccgcct cacccagtac ategacggge agggteggee ttegaaccca gecaagteag aagaagacce gggtetggea 780 cccgtcggga atggcaagtg gctcaatgtc cactatcact gctcaggggc cccctgcccg 840 900 caccgctgca gtgagctcag ccacaggggc ttttaggaga ttccagccgg aggtccgaac cttcgcagcc agtggctctg gagggcctga gtgacagcgg ccagtcctgt ttgtttgaag 960 gtttaaaaca attcaattac aaaageggca agcagecaat geacgeceet geatgeagee 1020 ctcccgcccg cccttcgtgt ctgtctctgc tgtaccgagg tgttttttac atttaagaaa 1080 aaaaaaaaag aaaaaaagat tgtttaaaaa aaaaaggaat ccataccatg atgcgtttta 1140 aaaccaccga cagcccttgg gttggcaaga aggcaggagt atgtatgagg tccatcctgg 1200 1260 catgagcagt ggctcaccca ccggccttga agaggtgagc ttggcctctc tggtccccat ggacttaggg ggaccaggca agaactctga cagagctttg ggggccgtga tgtgattgca 1320 1380 gctcctgagg tggcctgctt accccaggtc taggaatgaa cttctttgga acttgcatag 1440 gcgcctagaa tggggctgat gagaacatcg tgaccatcag acctacttgg gagagaacgc agageteeca geetgetgtg gaggeagetg agaagtggtg geeteaggae tgagageeeg 1500 gacgttgctg tactgtcttg tttagtgtag aagggaagag aattggtgct gcagaagtgt 1560 accegecatg aagcegatga gaaacetegt gttagtetga catgeactea etcatecatt 1620 tctataggat gcacaatgca tgtgggccct aatattgagg ccttatccct gcagctagga 1680 gggggaggg ttgttgctgc tttgcttcgt gttttcttct aacctgggca aggagagag 1740 caggecetgg geaaggetee egtgeegeet ttgggtteet tgttttettg ttgettgate 1800 1860 tggaccatct ttgtctttgc cttttcacgg tagggtcccc atgctgaccc tcatcttggg 1888 cctgggcctc ttgccaaagt tgcccctg

<210> 67

<211> 1712

<212> DNA

<213> Homo sapiens

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<400> 67
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                                                                       60
teeggeagae caaggatgee etetteacaa ttetecatga eeteegaeee caggacegtt
                                                                      120
teagtateat tggattttee aaceggatea aagtatggaa ggaceaettg atateagtea
                                                                      180
ctccagacag catcagggat gggaaagtgt acattcacca tatgtcaccc actggaggca
                                                                      240
cagacatcaa cggggccctg cagagggcca tcaggctcct caacaagtac qtqqcccaca
                                                                      300
gtggcattgg agaccggaga gtgtccctca tcgtcttcct gacggatggg aagcccacgg
                                                                      360
teggggagae geacaccete aagateetea acaacaceeg agaggeegee egaggeeaag
                                                                      420
tetgeatett caccattgge ateggeaacg acgtggaett caggetgetg gagaaactgt
                                                                      480
cgctggagaa ctgtggcctc acacggcgcg tgcacgagga ggaggacgca ggctcgcagc
                                                                      540
teategggtt etaegatgaa ateaggacee egeteetete tgacateege ategattate
                                                                      600
cccccagctc agtggtgcag gccaccaaga ccctgttccc caactacttc aacggctcgg
                                                                      660
agatcatcat tgcggggaag ctggtggaca ggaagctgga tcacctgcac gtggaggtca
                                                                      720
ccgccagcaa cagtaagaaa ttcatcatcc tgaagacaga tgtgcctgtg cggcctcaga
                                                                      780
aggcagggaa agatgtcaca ggaagcccca ggcctggagg cgatggagag ggggacacca
                                                                      840
accacatcga gcgtctctgg agctacctca ccacaaagga gctgctgagc tcctggctgc
                                                                      900
aaagtgacga tgaaccggag aaggagcggc tgcggcagcg ggcccaggcc ctggctgtga
                                                                      960
gctaccgctt cctcactccc ttcacctcca tgaagctgag ggggccggtc ccacgcatgg
                                                                    1020
atggcctgga ggaggcccac ggcatgtcgg ctgccatggg acccgaaccg gtggtgcaga
                                                                    1080
gcgtgcgagg agctggcacg cagccaggac ctttgctcaa gaagccatac cagccaagaa
                                                                    1140
ttaaaatctc taaaacatca gtggatggtg atccccactt tgttgtggat ttccccctga
                                                                    1200
gcagactcac cgtgtgcttc aacattgatg ggcagcccgg ggacatcctc aggctggtct
                                                                    1260
ctgatcacag ggactctggt gtcacagtga acggagagtt aattggggca cccgccctc
                                                                    1320
caaatggcca caagaaacag cgcacttact tgcgcactat caccatcctc atcaacaagc
                                                                    1380
cagagagatc ttatctcgag atcacaccga gcagagtcat cttggatggt ggggacagac
                                                                    1440
tggtgctccc ctgcaaccag agtgtggtgg tggggagctg ggggctggag gtgtccgtgt
                                                                    1500
ctgccaacgc caatgtcacc gtcaccatcc agggctccat agcctttgtc atcctcatcc
                                                                    1560
acctetacaa aaageeggeg ceetteeage gacaceacet gggtttetac attgecaaca
                                                                    1620
gcgagggcct ttccagcaac tgcagggtct tctgtgagtc tggcatcctg attcaggaac
                                                                    1680
tgacccagca gtccgtggca gttgctggtc ga
                                                                    1712
```

```
<210> 68
<211> 839
<212> DNA
```

<213> Homo sapiens

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<400> 68
gttttttctc gagcaggtta gccaatatac ctttgctatg tgcagttata gagaaaagaa
                                                                      60
gtctgaacca caagaattaa tgcagcttga aggctatact gtggattata ccgatccca
                                                                      120
eccaggeett cagggtggtt gtatgttett taatgetgtt aaagaaggag atactgtaat
                                                                      180
ctttgccagt gatgatgaac aggacagaat attatgggtt caagccatgt atagggccac
                                                                     240
aggtcaatca tataaaccag ttoctgcaat tcaaacccag aaactgaatc ctaaaggagg
                                                                     300
aactctccat gcagatgctc agctttatgc agatcgtttt cagaaacatg gtatggatga
                                                                     360
gtttatttct gcaaacccct gcaagcttga tcatgccttc ctttttagaa tactccagag
                                                                     420
gcagactttg gatcacagac tgaatgattc ctattcttgc ttgggatggt ttagccctgg
                                                                     480
ccaagtettt gtgttagatg agtactgtge ccgttatggt gtgagagget gtcacagaca
                                                                     540
tetetgetae ettgeagaae tgatggaaea tteagaaaat ggtgetgtea ttgaceetae
                                                                     600
cetgetecat tacagetttg cattetgtge etetegatgt geacggeaac aggeetgatg
                                                                     660
gaattgggac tgtttcagtg gaagaaaaag aaagatttga ggagataaaa gagagactct
                                                                     720
cttccctttt agaaaatcag ataagccatt tcagatactg ttttcccttt ggacgacctg
                                                                     780
aaggtgctct aaaagctaca ctttcattac ttgaaagggt tttaatgaaa gatattgcc
                                                                     839
```

```
<210> 69
<211> 801
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)...(801)
<223> n = a,t,c or g
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```
<210> 70
<211> 531
<212> DNA
<213> Homo sapiens
```

```
<400> 70
agaagggtgt cccaaccttg ctcatggcag ctggcagctt ctatgacatt ctggccatca
                                                                      60
ctggcttcaa cacatgcttg ggcatagcct tttccacagg ctctactgtc tttaatgtcc
                                                                     120
                                                                     180
tcagaggagt tttggaggtg gtaattggtg tggcaactgg atctgttctt ggatttttca
                                                                     240
ttcagtactt tccaagccgt gaccaggaca aacttgtgtg taagagaaca ttccttgtgt
                                                                     300
tggggttgtc tgtgctagct gtgttcagca gtgtgcattt tggtttccct ggatcaggag
                                                                     360
gactgtgcac gttggtcatg gctttccttg caggcatggg atggaccagc gaaaaggcag
                                                                     420
aggttgaaaa gataattgca gttgcctggg acatttttca gccccttctt tttggactaa
                                                                     480
ttgggagcag aggtatctat ttgcatctct cagaccagaa actgtaggcc tttgtgttgc
                                                                     531
caccgtaggc atttgcagta ttgatacgaa tttttgacta cattttctga a
```

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<210> 71
<211> 540
<212> DNA
```

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<213> Homo sapiens

<400>	71	•				
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<211> 428

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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tctggtggcc ggagtgatat tctgccataa acggcgagtc caaggggcta agggcttcca 300
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gtttggaaag	agtcagaaat	cttcacatac	gtgagctgaa	aagaataaac	aatgaagata	540
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gtagaggtgg	ctttagtgaa	gtgtataagg	taatgtatgg	tttattctgg	tttttttaca	660
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<210> 77 <211> 426 <212> DNA <213> Homo sapiens

<400> 77

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ggctccaggt gtaacctgcc cacctcagag gccacccacg cagtaacaga gggcagggga 360
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426

<210> 78 <211> 358 <212> DNA <213> Homo sapiens

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<210> 79 <211> 322 <212> DNA <213> Homo sapiens

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aattatcaga	ggatgttgaa	cagattgatc	acgctgatag	ggagttgcgg	cgtggccaaa	300
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<210> 85 <211> 342 <212> DNA <213> Homo sapiens

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atagacaagc	tggagctgct	ggctcccgga	tgaatttcag	acctggggtt	ctcagctcca	180
ggcaacttgg	actcccagga	cctcctgacg	gtcctgacta	tactgtttac	tacccgttcc	240
atcgacttgc	catggtgact	gctgcctcac	gattggagcg	tgaacacctt	acgcatctat	300
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<210> 87 <211> 392 <212> DNA <213> Homo sapiens

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535

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ggccagtatt	gatgctattt	tttcccttac	ctatcagact	ctttcaaaga	gaaaagaggg	180
agcagttgga	attttatgtt	tgttgttcta	ttttgtctat	tatgaattgt	gacaaaacca	240
ttataaaaga	tgacaagtgt	gtgtgtttct	ttttttcttt	ttaaactgta	gggaacatag	300
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<210> 90 <211> 432 <212> DNA <213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<220>

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<223> n = a,t,c or g

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                                                                     120
cagaaaatga aggtagttgt cacagtgatc agatgagcaa cgatttctcc aatgatgatg
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aacgagaaat tgagcgcaat acatgcaaga taaaattatt ctgtttgcat cctacaaaac
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aagtaatgat ggaaaantaa attgaggttc ataaggataa gacattaaag gaagcagtag
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<210> 92

<211> 867

<212> DNA

<213> Homo sapiens

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                                                                     780
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<210> 93

<211> 690



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<210> 95

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<212> DNA

<213> Homo sapiens

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value nome supreme

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2191

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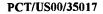
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	tattttaatt					300
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	gttgcatggt					540
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	cgaggtggtg					780
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	tccaattggt					240
	cgacctttaa					300
	tgtgttactc					360
	ageggeaaca					420
	ttctcctctt					480
	tccaggccct					540
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<213> Homo sapiens

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gaagaaagac	aagaaggacc	tgagatagag	tttgggtttt	ccttttttc	tetetetett	180
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<210> 117
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<212> DNA
<213> Homo sapiens
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<212> DNA

<213> Homo sapiens

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ggcccggcgc	aggtgttcca	ggagaccatg	aactcgcagg	tgatcctgat	tattgccgcc	720
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<210> 119

<211> 427

<212> DNA

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#### <213> Homo sapiens

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cggcagagaa	gaaatccgtc	ttcatattgt	ttgcgatgtc	cctgatgaac	240
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<213> Homo sapiens

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caaactgatc attcagggcg aaccggatat gccgattgtc agagtcggtg cgcgcttgct 180
gtataactat ctggttaaag gcggcgttca ggtttttgag taccgccgcc gcccgctcca 240
cggcaaagtg gcattgatgg acgatcactg ggcgacagta gggtccagta atctccatcc 300
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<210> 122 <211> 724 <212> DNA <213> Homo sapiens

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<213> Homo sapiens

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	tattttaaaa					180
	aggagaatcc					240
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<210> 124 <211> 363 <212> DNA <213> Homo sapiens

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<213> Homo sapiens

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<210> 126 <211> 362 <212> DNA <213> Homo sapiens

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<210> 127 <211> 351 <212> DNA <213> Homo sapiens

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<210> 128 <211> 374 <212> DNA <213> Homo sapiens

<400> 128
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<210> 130 <211> 359 <212> DNA <213> Homo sapiens

465

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<210> 133 <211> 354 <212> DNA <213> Homo sapiens

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180

210

780

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ccg						963

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<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
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<223> n = a,t,c or g
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<210> 139

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gctttaggaa aggaaagcca tcagcaggga	gaagacacaa					360 376

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<211> 968
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)...(968)
<223> n = a,t,c or g
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<210> 140

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                                                                      120
                                                                      180
ggggctggca gtccctgagc tttgatggcg gggccttcca ccttaagggc acaggagagc
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tgacacgggc cttgctggtt ctccggctgt gtgcctggcc cccactcgtc actcacgggc
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tgttgctcca ggcctggtct cggcgactcc tgggctcccg gctctcaggc gcatttctcc
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                                                                      540
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                                                                      720
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<210> 141

<211> 306

<212> DNA

<213> Homo sapiens

<400> 141

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atcagtaggg gaagagaaaa gatgggcaat atgtatagtc agacgagaa	
cagagggctc atggagaagt aggctaccca ccacataacc ccatcatag	
atacagetat agataagaat atecaceagt eggtgagtga geagateaa	
ccaaqa	306

<210> 142

<211> 316

<212> DNA

<213> Homo sapiens

<400> 142

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tacattctta	ttattgcaca	acaaatagaa	gactttggat	ttccttatat	aagtaccttg	180
acagatgact	aacccatttt	tcctatgctt	tacaactatg	atcagtaact	gtaattttt	240
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<210> 143

<211> 339

<212> DNA

<213> Homo sapiens

<400> 143

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,	gaattatagc	ctcattttt	cttagaacct	ttatattttg	ttttattcat	atacagggtt	240
1	gtcaagctgg	acagactatt	aaagttcaag	tctcctttga	tttgcttagt	ctgatgttta	300
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<210> 144 <211> 2018 <212> DNA <213> Homo sapiens

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<210> 145

<211> 429

<212> DNA

<213> Homo sapiens

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<210> 146 <211> 717 <212> DNA <213> Homo sapiens

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<210> 147 <211> 367 <212> DNA <213> Homo sapiens

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<211> 791
<212> DNA
<213> Homo sapiens

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<223> n = a,t,c or g
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<210> 149 <211> 335 <212> DNA <213> Homo sapiens

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tgacagcaaa	cttctaaagt	gggctgtgag	gtagggaggg	gacacaagcg	ttttgaggct	300
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349

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	agggagcgcc					480
	atattgtgac					540
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<210> 151 <211> 349 <212> DNA <213> Homo sapiens

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tgtagtcata aagcagaatt acacatcaag aaagataact tactaaacaa aaacaacaga 240
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<210> 152 <211> 324 <212> DNA <213> Homo sapiens

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<210>	153					
<211>	377					
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atcacaqtta	atatttattg	agagtttaaa	tatgtgccca	cagattagat	tacctatttt	180
	ttttaatttt					240
tttqccaaqt	attttcacat	gtacttattt	cactgctatt	ctctacaata	gtcttgtgac	300
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<210> 154 <211> 1224 <212> DNA <213> Homo sapiens

<213> Homo sapiens

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<210> 155
<211> 345
<212> DNA
<213> Homo sapiens
<220>
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<222> (1)...(345)
<223> n = a,t,c or g
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cagcagcaaa	tgttacaaca	agagacaatt	agaaatggag	agctagaaga	tactcaaact	180
aaacttgaaa	aacaggtgtc	aaaactggaa	caagaacttc	aaaaacaaag	ggaaagttca	240
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<210> 156 <211> 340 <212> DNA <213> Homo sapiens

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<210> 157
<211> 478
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<213> Homo sapiens
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<222> (1) ... (478)
<223> n = a,t,c or g
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<400> 157
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gagcctgcac	ctgacccccc	ggggcctcat	ttcctccggc	aggagcgcag	cttcgagtgc	180
cgcatgtgcg	gcaaggcctt	caagcgctcg	tccacgctgt	ccacccacct	gctcatccac	240
tcagacacgc	ggccctaccc	ctgccagttc	tgcggcaagc	gtttccacca	gaagtccgac	300
	acacctacat					360
	gccagagctc					420
tgctgtctcc	tgccgacaag	accaacgtca	aggccgcctg	gngtaagggt	cgcgcgca	478

<210> 158

<211> 332

<212> DNA

<213> Homo sapiens

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aagtggcagc	cagcaccgca	ccaagtctgt	ttgggcagca	gactggtatc	acagccagca	120
	cactccacag					180
tagtattatt	gaatatatat	aatgttttat	atattagact	ttatacttga	gacataggaa	240
ataatttatg	tataactgtt	aattaaattt	tatatttgct	agattagaaa	attctattaa	300
tttattaatg	aattatatct	aattatgtga	ca			332

<210> 159

<211> 868

<212> DNA

<213> Homo sapiens

#### <400> 159

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                                                                     120
aactgcatac aagttataaa gtttaataat ctttatcatc ttggaaaata aatctcttct
                                                                     180
tgctaagtat cagtttttaa aaattgcccc atgtattaga tatgtatttt tttaacaaaa
                                                                     240
atgttctgtg tattaattat tttgaaataa attttaagtt cacaaaaagc cattacaaga
                                                                     300
agtggaaata gcagcaatta cacatggtgc tcttcaggga ttagcctact tacattctca
                                                                     360
tactatgatt catagagata tcaaagcagg aaatatcctt ctgacagaac caggccaggt
                                                                     420
gaaacttgct gactttggct ctgcttccat ggcatcacct gccaattcct ttgtgggaac
                                                                     480
gccgtattgg atggccccag aagtaatttt agccatggat gaaggacaat atgatggcaa
                                                                     540
agtagatgtg tggtctcttg gaataacatg tattgaacta gcggaaagga agcctccttt
                                                                     600
atttaatatg aatgcaatga gtgccttata tcacatagcc caaaatgaat cccctacact
                                                                     660
acagtctaat gaatggtgag tattgttaat atatatattg ctcagtgttg aataaatgaa
                                                                     720
atgettttte ataatetgtt atcaaagtga tttaatttea gttaggtaaa atgtateace
                                                                     780
ttataagata ttaaaataga tgtattttac ccttttaaat atatttattc tttatcatgt
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<211> 1404 <212> DNA

<213> Homo sapiens

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<210> 161 <211> 562 <212> DNA <213> Homo sapiens

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<211> 1812

<212> DNA

<213> Homo sapiens

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                                                                     180
cagatggtac ggccatgccg gtcctgcagg gagctcatgc ctggcatgcc atagcagcgc
agecaggete gaaaggeage aaagteetee teeeegetet etgaceegta geceetgeee
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                                                                     300
cccaactgga ccacttcctt gggcactgag tgacataget ccagcaggtc tggattctgc
                                                                     360
agettggtcc ttatettetg getcagggtc agetcegggc teggectgtg ctgctgcagg
gcetccagga ccgagcgggc cttctcaaag ggggggatet tcagccggta caggatetet
                                                                     420
                                                                     480
gcccgcagat agttgccaat gccattgaag aacctctggt ccaggagggc ctcgcagatg
                                                                     540
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tectgeaaga cacagggeee geggeeegge tgecaettte ceccaaggte ceageggeeg
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                                                                     660
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                                                                     780
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                                                                     900
aagggcacct cagggttgcg gctgacagag gactteteca cgcagecgce gaacaceage
                                                                     960
gccctgcagg cctcattcac aaactggctg gccaggtgca gctcggggcc ctcaggcatc
ctgagggagg gtggcagagt cctggctggg aggtggcgga agaacctgac ttcccactgc
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                                                                    1200
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                                                                    1560
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aggteeggtt gggeeteggg agggeeteeg tgtggagtet geaetteatt etaagtgtat
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qcqtaataaa attatqtqqc tttqtaaqaa attggttttt agagatgcat gttaaagtat
                                                                    1740
tgggtatgaa atgtcatgat ttgtctaatt tactttaaaa tacttctgcc ataataaatg
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                                                                    1812
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<210> 163
<211> 333
<212> DNA
<213> Homo sapiens
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gcaacactgg actgtcatcc caaggettat tgatatttgc ggagttgatt cctgccatta
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ctcatttagg aacaggcatg caccgtgtga tcggactgat gcttctatac ttaatctttg
300
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333
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<210> 164 <211> 134 <212> DNA <213> Homo sapiens

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<210> 165 <211> 839 <212> DNA

<213> Homo sapiens

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<210> 166 <211> 1256 <212> DNA <213> Homo sapiens



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cccctttgac ctgggcaacc	agctgctggg	actgaaaggt	gtgatggaga	tgatggtggc	480
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catcetgtac teggtggcca					960
ggtcatccca gagcttgtcc	agctcgccaa	gttctccaag	cagcatgtgc	ccgaggaaca	1020
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<210> 167

<211> 892

<212> DNA

<213> Homo sapiens

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	gcgagaccct					180
	gacactgtcc					240
	ccgcgagtgc					300
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teccageeeg	gacacccctt	tttaagatta	acttectqca	gctacccagg	gacttcccgg	420
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	ccgagcgttg					600
	atttcttcag					660
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actacaacac	cctgcggcac	cragradece	accegeeag	ggtggetgea	cyatttatyy	892
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<210> 168

<211> 394

<212> DNA

<213> Homo sapiens

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caggggaccc	tttctgaccg	acaagaaacc	gtggtcagga	ccgagggtgg	ccctcaggcc	240
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<213> Homo sapiens

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<210> 170 <211> 422 <212> DNA <213> Homo sapiens

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<210> 171 <211> 1042 <212> DNA <213> Homo sapiens



<400> 171 eggacgegtg gggteatgga getggeaetg eggegetete eegteeegeg gtggttgetg 60 ctgctgccgc tgctgctggg cctgaacgca ggagctgtca ttgactggcc cacagaggag 120 ggcaaggaag tatgggatta tgtgacggtc cgcaaggatg cctacatgtt ctggtggctc 180 tattatqcca ccaactcctg caagaacttc tcagaactgc ccctggtcat gtggcttcag 240 300 ggeggtecag geggttetag cactggattt ggaaactttg aggaaattgg geeecttgae agtgatetea aaccaeggaa aaccaeetgg etecaggetg eeagteteet atttgtggat 360 aatcccgtgg gcactgggtt cagttatgtg aatggtagtg gtgcctatgc caaggacctg 420 gctatggtgg cttcagacat gatgggtctc ctgaagacct tcttcagttg ccacaaagaa 480 ttccagacag ttccattcta cattttctca gagtcctatg gaggaaaaat ggcagctggc 540 attggtctag agctttataa ggccattcag cgagggacca tcaagtgcaa ctttgcgggg 600 gttgccttgg gtgattcctg gatctccct gttgattcgg tgctctcctg gggaccttac. 660 ctgtacagca tgtctcttct cgaagacaaa ggtctggcag aggtgtctaa ggttgcagag 720 caagtactga atgccgtaaa taaggggctc tacagagagg ccacagagct gtgggggaaa 780 gcagaaatga tcattgaaca ggtaaaaagg ggaaacactc agaggcgagc ctgcttggct 840 ttttctggtg ggtacagggc ccatggttgg tgttgtcaaa cttggagtct acactgaggc 900 tocccacata totgcaaatg attgcatgot ggataataaa totottgggt otaagcagtg 960 atgtagtggc tccttacaga gtcagaaagc cacccaggcc tgcaagactt gcttgtcctt 1020 cactaaatgt aaaaattcta tt 1042

<210> 172 <211> 890 <212> DNA <213> Homo sapiens

<400> 172 aaagtagtag gttggtgcaa acgtagtaat aaattggttt ggccctgttt tcatagaact 60 atagaggttg gacctttgtc cccttccaga tgcctacaaa caaactgatg tttttgattt 120 ttttttttttt ttaaattttg gttgccacta attcttataa aaatcctcac acaaggctgg 180 gctcagtggc tcacacctgt aatcccaqca ctttgggagg ctgaggcagg cggatcacga 240 ggtcaggaga tcgagaccat cctggctaac acggtgaaac ccccgtctct actaaaaata 300 caaaaaaatt agccgggcgt ggtggcgggc gcctgtagtc ccagctactc gggaggctga 360 ggcaggagaa tggcgtgaac ccgggaggca gagcttgcag tgagccgaga tagcgccact 420 480 ctgtaatccc agcactttgg gaggccgagg caggcggatc acgaggtcag gagatcgaga 540 600 ccatcctggc taacacggtg aaaccccgtc tctactaaaa atacaaaaaa ttagctgggc gtggtggcgg gcacctgtag tcccagctac ctgggaggct gaggcaggag aatggcgtga 660 720 acccaggagg cggagettgc agtgagegga gatcatgeca ctgcacttca gcctgggcga 780 840 atagaaaaat aataatagtt ttaagcacct ctaaagtaca gatattgtgc caagcaattt 890 atgtgaattg attagattga taactctaaa aatagtttcc ctaatcaact

<210> 173 <211> 1922 <212> DNA

<213> Homo sapiens

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tcatcaattg	cttcatcaaa	ctcatcaaat	ctgtagctta	tacatttcct	tgttcttgtt	180
gacctccttt	caaagcaagt	ttgctttgga	tttttttgaa	tctttttct	tttcttcttg	240
	aagtctggct					300
tacaccaagc	gttcttttcc	ttcgttccgg	caacgctctt	tccttctta	aggcaacatc	360
ccaaatcctg	gaaactggtc	ctctaatttt	tccaacaaga	gcaagtttaa	tgttgggcaa	420
aaggtggggc	aagaacccat	cctcccatct	ggggatggat	catcagagga	ggggcgaaag	480
gcagggcagt	atggtatcca	ctatcgcaag	agtcacacag	aagaattagc	tcaggatggt	540
ttggaaggcc	acattttttg	catggttcat	catcatctgc	taggatggct	tcttcacttt	600
ccttttcttc	ctcctcttct	gaagctgcag	atgattttc	actgccagac	ccttcacttt	660
catcattgct	ggaatatttc	catctgccac	gtgtccgaga	accagtccat	cgaactttgc	720
ctttgggttt	taccttgctt	actttagaat	ttgtatcttt	ctctgatttt	ttcaaaattt	780
cctttttgtc	agttttttgc	aaagctgttg	actcttcttc	cacctcatct	teteetteee	840
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ttcttggaga	tcttcttaaa	gtacgaccca	catttgtttt	ctcctcttcc	ttttctgtct	960
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actcggtgga	agataaagca	gtttttgaag	agagatettt	tgccatctca	gaagaatcaa	1620
gagaagtttc	catttctgga	ggatcgggtt	cctctatttg	tgctttttga	ctatggatct	1680
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cacctgtttt	catacttggt	tatgacagaa	tttaaggact	ctgttccatt	tccctccgtg	1800
	tgtccttagg					1860
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ca						1922

```
<210> 174
<211> 537
<212> DNA
<213> Homo sapiens
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#### <400> 174 aaaagcggcg cggctcgttc aagatggcgg agctcgacca gttgcctgac gagagctctt 60 cagcaaaagc ccttgtcagt ttaaaagaag gaagcttatc taacacgtgg aatgaaaagt 120 acagttettt acagaaaaca eetgtttgga aaggeaggaa tacaagetet getgtggaaa 180 tgcctttcag aaattcaaaa cgaagtcgac ttttttctga tgaagatgat aggcaaataa 240 atacaaggtc acctaaaaga aaccagaggg ttgcaatggt tccacagaaa tttacagcaa 300 caatgtcaac accagataag aaagcttcac agaagattgg ttttcgatta cgtaatctgc 360 tcaagcttcc taaagcacat aaatggtgta tatacgagtg gttctattca aatatagata 420 aaccactttt tgaaggtgat aatgactttt gtgtatgtct aaaggaatct tttcctaatt 480 tgaaaacaag aaagttaaca agagtagaat ggggaaaaat tcggcggctt atgggaa 537

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<210> 175
<211> 659
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)...(659)
<223> n = a,t,c or g
```

#### <400> 175 tetetetttg ecagtaatgt tggaagtgga cattteattg geetggeagg gteaggtget 60 gctacgggca tttctgtatc agcttatgaa cttaatggct tgttttctgt gctgatgttg 120 180 240 eggaageget teggtggeat cagaateece ateateetgg etgtaeteta cetatttate 300 tacatettea ceaagatete ggtagacatg tatgegggtg ceatetteat ceageagtet 360 ttgcacctgg atctgtacct ggccatagtt gggctactgg ccatcactgc tgtatacacg gttgctggtg gcctggctgc tgtgatctac acggatgccc tgcagacgct gatcatgctt 420 480 ataggagcgc tcaccttgat gggctacagt ttcgccgcgg ttggtgggat ggaaggactg 540 aaggagaagt acttettgge eetggetage aaceggagtg agaacagcag etgegggetg cccegggaag atgcctttca tatttttcga gatccgctga catctgatct cccgtggccg 600 ggggtcctat ttggaatgtc catcccatcc ctctggtact ggngcacgga tcaggtgaa 659

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<210> 176
<211> 1033
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)...(1033)
<223> n = a,t,c or g
```

```
<400> 176
cccacgcgtc cggatgtgtg ctcacacttg ggggacctga ttggggcttc agaccttggg
                                                                      60
                                                                     120
ggcctgtccg cagggtctcc tccatccttc ttgatttgcc tgtcattgag gctgcccgct
                                                                     180
ctgggcgcca ttccccagcc taacacctct tctcagtctt tccttgcagg tccctggagt
ccaggccttg gggcagtgaa gaaaccgtgg ggaggggcat gagatgccag tccccaaagt
                                                                     240
ccttgggagc ccttgtgggc caagtcattg taggacacac cctctcctgg gcattgctga
                                                                     300
ggtcacccag tgagcctagg ctccccctc ctcccatccc cagcctgggg gaaccttcag
                                                                     360
egteteteet eeetgtagge eeeggeteag etteeeagga aettttgttg gtgggtaeta
                                                                     420
gtagggtaag gcagttette ceateatgag ggagaeettg ggagaettte attaccaaat
                                                                     480
ccattgctgc cccgacette ctgggactga tctgggtcac cctggtctcc tgatcttgga
                                                                     540
gaagtcaagt tettateeca gaettgagag gttacaagee tecaggtete tggcaaagtg
                                                                     600
                                                                     660
tggagatgat ggacagccat ttgtacacac accagccagt cccttagcat atctctcttg
                                                                     720
gttttgtete aggtetgeet cagecacete cetgaegetg teccaetgtg tggatgtggt
                                                                     780
gaaggggett etggatttta agaagaggag aggteaetea attgggggag eeeetgagea
gegataceag atcatecetg tgtgtgtgge tgeeegaett eetaeeeggg etcaggatgt
                                                                     840
getgeageet cetggeeact ggaggggetg accgeetgat ceacetetgg aatgttgtgg
                                                                     900
                                                                     960
gaagtegeet ggaggeeaae eagaeeetgg agggagetgg tggeageate accagtgtgg
                                                                    1020
actttgaccc ctcgggctac caggttttag cagcaactta caaccaggtt gcccagtttt
                                                                    1033
ggaaggtngg gga
```

```
<210> 177
<211> 335
<212> DNA
<213> Homo sapiens
```

<400> 177
gtcaaaaacg atttcctagc aactgtggcc gtgatggaaa actgtttctt tggggacaag 60
cacttcatat catcgcaaaa ctcctgggta agtggagaag attgggaatg gtatttttt 120
ccttgttatt aagctattag aaataaatat gcctttgctg gcacataata gtactttggt 180
acaacaggat atcctatgga gtttaaaaat aagtatttaa aatataacaa atctgtatta
gtccattctc atgctactaa taaagatata cccaagactg ggtaatttat aaaggaagga 300
gttttaatgg cctcacagtt ccgtcgacgc gggcg
335

```
<211> 556
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)...(556)
<223> n = a,t,c or g
```

<210> 178

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<400> 178
gttcacgtct gcagcagtaa gatgggagct ttgtccacgg agcggctaca gtactacact
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caggaactgg gggtccggga gcgcagtggc cacagcgtgt ccctcatcga cctctggggc
                                                                      120
ctccttgttg agtatctcct gtaccaggag gagaaccctg ccaagctgtc tgaccaacag
                                                                      180
gaggeggtee gecagggtea gaaccettae cecatttaca ceagtgteaa egteegeace
                                                                      240
aacttgagtg gggaagattt tgcagagtgg tgcgagttca cgccctatga ggttggcttc
                                                                      300
                                                                      360
cccaagtacg gggcttatgt tcccaccgag ctcttcggct cagaactctt catgggacga
                                                                      420
ttgctgcagc tccagcctga accccggatc tgttacctgc aaggtatgtg gggcagcgcc
                                                                      480
tttgccacca gcctggatga gatcttccta aagaccgccg gctcgggcct cagcttcctg
                                                                      540
gagtggtaca gaggcagtgt gaatatcaca gacgactgcc agaagcctca gctgcacaac
                                                                      556
ncctcgacgc gggaat
```

```
<210> 179
<211> 631
<212> DNA
<213> Homo sapiens
```

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<400> 179 gaatttetgg gtcgtcccac gcgtcccgca aaggatgagg gaaacgatga gggaaaggat 60 gagggaaagg atgagggaaa ggatgaggga aaggatgagg gaaaggatga gggaaaggat 120 gagagaaagg atgagggaaa ggatgaggga aaggatgaga gaaaggatga gggaaaggat 180 gagggaaagg atgagggaaa ggatgaggga aaggatgagg gaaaggatga gggaaaggat 240 300 gagggaaagg atgagggaaa cgatgaggga aaggatgagg gaaaggatga gggaaaggat gagggaaagg atgagggaaa ggatgaggga aaggatgagg gaaacgatga gggaaacgat 360 420 gagggaaacg atgagggaaa ggatgaggga aaggatgaga gaaacgatga gggaaaggat gagggaaagg atgagggaaa ggatgaggga aaggatgaga gaaacgatga gggaaaggat 480 gagagaaagg atgagggaaa ggatgaggga aaggatgagg gaaaggatga gggaaaggat 540 gagggaaagg atgagggaaa cgatgaggga aaggatgaga gaaaggatga gggaaaggat 600 631 gagggaaagg atgagggaaa ggataagtaa g

<210> 180
<211> 469
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1) ... (469)
<223> n = a,t,c or g

<400> 180 ggcggggctc ntttgagacc tgatgaccat cattacgccc agcttggcac gagggggagg 60 acttcagcta cggcctgcag ccctactgcg ggtactcctt ccaggttgtg ggggagatga 120 180 teeggaaceg ggaggtgetg eettgeeeeg atgaetgtee egeetgggeg tatgeeetea tgatcgaggg ctggaacgag ttccccagcc ggagggcccg ctttaaggac atccacagce 240 ggetecgage etggggeaac etttecaact acaacagete ggagcagace teggggggca 300 360 gaaacaccac gcagaccage teeetgagea ccageccaet gtgcaatgtg agcaacgeee 420 cctacgtggg gcccaagcag aaggtcccgc cctttccaca gacccaggtc atccccatga 469 agggccagat cagacccatg gtgcccccgc cgcagctata cgtccccgg

<210> 181 <211> 453 <212> DNA <213> Homo sapiens

<400> 181 caggaattcc gggcgccacc cacgcgttcg atggatcctg gaagagcgca agcgggtgat 60 geaggaggee tgegeeaagt acegggegag cageageege egggeegtea egeeeegeea 120 . 180 cgtgtcccgt atcttcgtgg aggaccgcca ccgcgtgctc tactgcgagg tgcccaaggc 240 cgacatccag cacaacaccg tccactatgg cagcgctctc aagcgcctgg acaccttcga 300 360 ccgccagggt atcttgcacc gtctcagcac ctacaccaag atgctctttg tccgcgagcc cttcgagagg ctggtgtccg ccttccgcga caagtttgag caccccaaca gctactatca 420 cccggtcttc tgcatggcca tactggcccg gta 453

<210> 182 <211> 377 <212> DNA <213> Homo sapiens

	<400>	182		•			
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г	gtcaaggat	gatgtgaact	tggatacagt	acttctccta	ccctttttga	aagaaatagc	120
		ctggatcaac					180
C	attggtcac	tccttccata	tagatttgct	gcagcacctc	ctgcctggct	gggataaaaa	240
t	aagctactt	caggtcttga	gagctcttgt	ggatatacat	gtgctctgct	ggtctgacaa	300
9	gagccaagag	cttcctgctg	agcccatatt	aatgccttcc	tctatcgaca	tcattgatgg	360
a	accaaagag	aagaaga					377

<210> 183 <211> 621 <212> DNA <213> Homo sapiens

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<400> 183
ctcatcctta aagtgacaga gtaaattaac tctaaggccc catccaggac tcaagctgtg
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                                                                     120
aagagactag cagaaagaca ggtgggtgat gggatgtcct ggacagagcc tggatcatga
                                                                     180
ggtccccatg tagtgcttgt actacgcaga tgtttcctct tgagctattt taaaggtgtg
                                                                     240
gaaaaagcca aagcaatgcc ctctccacgg atactaaaga ctcacctttc cactcagctg
                                                                     300
ctgccaccgt ctttctggga aaacaactgc aaggtaagat accaacagct ccctgtgaca
                                                                     360
gaagggaaag taagccaacc aaagcgagtc ctgcagaccc caacgcagag cattcgtgat
                                                                     420
cacctttgcc tctccactgt ctctgatgct taccagcaaa gagaaaacat aaagttctac
                                                                     480
attcagcagg acattcacct gaacagtttc aaataggaca tgaaggcagg atccagattg
                                                                     540
aatgtttgga gggaactaga gacatgggga ggcagtgagt gcagtaagcg tagctgtgaa
                                                                     600
atgaagggga gaagatggtg g
                                                                     621
```

<210> 184 <211> 415 <212> DNA <213> Homo sapiens

<400> 184
accgggacga cccacgcgtc cgggaattta attctattat atatgcagac tttctaaaga

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agataaagct	tttttatggg	agaaacgtta	ttattgcttc	aaacacccaa	attgtcttcc	120
taaaatatta	gcaagcgccc	caaactggaa	atgggttaat	cttgccaaaa	cttactcatt	180
gcttcaccag	tggcctgcat	tgtacccact	aattgcattg	gaacttcttg	attcaaagta	240
agtcaaatac	atttatttgc	tcttgtttta	ttgtcagttt	ttccagtaag	gtatgttgcc	300
agaagtattt	cctttccttt	taacatgaaa	gcaattcaat	ataatccaaa	tgtgtaaatg	360
tatatttata	caaacatatc	ttctgcattg	aagttgtcaa	taaagcattg	catgt	415

<210> 185 <211> 359 <212> DNA <213> Homo sapiens

<400> 185 ggaaaatgat gatttgaggt ttatttgaaa tacaacaatg tccaatagga aaacactgca 60 actttettea ggtgttgaga aatecaatag agacetetge ttgteteete etttggeaag 120 agctccaagg ggagagaga gatgggccac cacgatgaat actacaggct gcggggaagg 180 ataaccctag tecagaccat tectacaaaa gaaatgggga ateegaaagg aaaaggaaga 240 aatctcacta gcacatgtca aagagccagg agaggcacaa ttcaccaagc agaggaagaa 300 atagtgaccg cagcgggggc cggtgcagcc gcagtgataa cggtcggagc cgttacagg 359

<210> 186 <211> 1616 <212> DNA <213> Homo sapiens

<400> 186 ggaggttgcg gcggcggctg cggcgcagcc cggggcggcg ggtgggaaga ggactaccag 60 120 aggggcctgc gggagaccca gggtcggacc cataggagtc ctgtcgtcag gacctccttg 180 ateggtette tgettgggtt eteggtgaag gaggagette ggggtgtegg etgggetgeg 240 eggacteete ttgggateeg atgatggate ecaceeggtg ategggaatg gggttacaat 300 gcagtgaggc ggaaaggctc tcgccggggc acagaaagat ccccagggcc gcaaggcgtg 360 ctgtcgcctg caaaggcact gacccacgag cccactgcct ccctccttcc tgggtggagc aggggeetge etteatetee aaggeeeggg ggeteeggea tetegaegeg getteeggeg 420 480 acacgggcaa agagagacag aggctagtcc gagccggagc cagtgtgacc acacgtggca etgacgtccc ccaagagcac atgcagtgag cctgtgtctc tgaggccgta gtgggcgacg 540 600 acgagacgga cagtgatgtc caggcctgcg cccgggggcc actggagacc tgcccctcaa 660 ageggaggaa aegecaaget cacetgaaaa eetgegagae agggeetgtg caegagteea 720 gtactcctac ttcgccaagt ctcagggacc catccccgag caacggtggc ggcgcagaga 780 agagcacggc gccggcgcag gtgcagagag acaggaggct gatgggggga agttgaggca cctggggcag agaaaaaat gcattgccaa gaggtttctg ggtcatctac tgacgaaaat 840 gtottcccat cagcccttgc gctggtcccc agggaccctg gcatccgtcg ttggcgccca 900 960 gggtgcgcgt cgggccacta ggggtacccc aactcggaca gaaggcccat gagttgaatt 1020 tgaagtttgt gggaatagag gtgaggcacc aggggcagaa aaaaaacagg agacctcgcc tcagacaagc ggggcctggg tcccccatgg atgaaagtgc cttcccatta tgctgtaccc 1080 1140 tgggcagagt ggacagtgac gaccetggtt cgageceagg gtgegetteg ggacegettg 1200 eggttaccag aaagegaaca aatggtecat gageggaagg tgaggeacet gaggeagaga 1260 aagtaaagaa acgcgccgcc gagaagcagt gcctgggtcc ctcacggagg aaattgtctt ctccttagcc cgttcgcttg gcagtgaggt ccctggcgtc cctggtttga tcccagggta 1320

cgcctcgggc	cactagtgtt	accccaaggt	gggcagaaag	cccataaggg	gaaggcgagg	1380
cacctggggc	agagaaaaaa	aaaaacttcg	ccgcaaagaa	gcgcggcctg	attccccacg	1440
gacgaaagtg	tcttcccatc	agtccctgca	ctgggacccg	gggaccctgg	tgtccctggt	1500
tcgagctcag	ggtgtgcctc	agccgctacg	tgcaccccaa	ggggagcttt	gggagcccaa	1560
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<210> 187 <211> 916 <212> DNA <213> Homo sapiens

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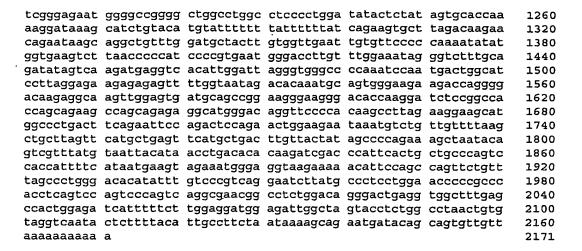
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				taatctgcag		300
gagatgcaaa	gcagctggct	ggaatgatca	cctttacctg	caacctggct	gagaatgtgt	360
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<210> 204 <211> 706

<212> DNA

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<210> 205 <211> 852 <212> DNA <213> Homo sapiens

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                                                                      180
tattettttg aaatggtgea geeagatttt gagttgeatg ceateagtgg ggaaattaea
                                                                      240
aatactcatc agtttgacag ggagtctctt atgaggcgga gagggactgc tgtgtttagc
                                                                      300
tttacagtca tagcaacaga tcaggggatc cctcagcctc tcaaggatca ggccactgta
                                                                      360
catgtttaca tgaaggatat aaatgataat gctcccaaat ttttaaaaga cttttaccaa
                                                                      420
gctacaatat cagaatcagc agccaatctg acacaagtgt taagagtatc tgcctcagat
gttgatgaag gtaataatgg acttattcac tattctataa taaaaggaaa tgaagaaaga
                                                                      480.
cagtttgcta tagacagtac ctctggtcag gtaacactaa ttggcaaatt agactatgaa
                                                                      540
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					cccctcaat	600
tcaacgtgta	ctttaaatat	tgatatttta	gatgaaaatg	acaatacccc	tttctttccc	660
taaatcaaca	cttctttgtt	gatgttttgg	aaaacatgag	aattggtgaa	ctcggggcct	720
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ttggcccaaa		_				852

<210> 206 <211> 361 <212> DNA <213> Homo sapiens

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aaaatcctct gaactgtgca gatcctactt ctcaaaggtg gtttcatgga cacctctctg 180
gaaaagaagc agagaaattg ttaactgaaa aaggaaagca tagtagcttt cttgtacgag 240
agagccagag ccaccctgga gattttgttc tctccgtgtg caccggtgat gacaaaggag 300
agagcaatga cggcaagtct aaagtgactc atgtcatgat tcactgtcag gaactgaaat 360
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<210> 207 <211> 2483 <212> DNA <213> Homo sapiens

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#### PCT/US00/35017 WO 01/53455

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<210> 208

<211> 366

<212> DNA

<213> Homo sapiens

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<210> 209

cggtgc

<211> 574

<212> DNA

<213> Homo sapiens

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gaatagtgaa	ggtgcattct	ccatccacaa	tcacgtggca	gacaatgtgt	tgctggaaaa	540
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<210> 210
<211> 383
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
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<223> n = a,t,c or g
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ggcacagatg tcccagtgaa agaacttctg aagaccatcc ccaaatacaa ggtaatgaat 180
gacctaatcc ctgaaatcaa agcaacagag atgcccagag ccttgtttc acaaagttca 240
ggcttcaaac tctactttgg agcgatgtt ttgctcacca ctattacagc ctgttagctt 300
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<210> 211 <211> 592 <212> DNA <213> Homo sapiens

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<213> Homo sapiens

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                                                                     120
ctttgcagga gccatgtaca tcctgggcac catcgaaatc ctgctggctt acctcttccc
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agccatggcc atcttcaagg cagaagatgc cagtggggag gcagcagcca tgctgaacaa
                                                                      240
catgcgtgtt tacggcacct gtgtgctcac ctgcatggcc actgtggtgt ttgtgggtgt
                                                                      300
caagtatgtc aacaagtttg cccttgtctt cctgggttgt gtcatcctct ccatcctggc
                                                                      360
catchatget ggggtcatca agtetgeett cgacccaccc aactteccga tetgeeteet
                                                                      420
gggtaaccgc acgctgtctc gccatggctt tgatgtctgt gccaagctgg cttgggaagg
                                                                      480
aaatgagacg gtgaccacac ggctatgggg ccttttctgc tcctctcgct tcctcaacgc
                                                                      540
cacctgtgat gaatacttca cccgaaacaa tgtcacagag atccagggca tccctggtgc
                                                                      600
tgccagtggc ctcatcaaag agaacctctg gagctcctac ctgaccaagg gcgtgattgt
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                                                                     1080 .
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                                                                     1320
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catgiticate tgetectggt attatgeact ggtagecatg cteattgetg gaeteateta
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gaacttcatt gagctggtcc gggaaaccac agctggccac ttagccctgc tggtcaccaa
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gaacgtttcc atgtttcctg ggaaccctga gcgcttctct gaaggcagca tcgaccgttg
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ggggattggg cacgatggag gcatgctcat gctggtgccc ttcctgctgc ggcaccacaa
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catgag
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<210> 213

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> n = a,t,c or q
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tcatcggcag	aaatacaaat	atttactcaa	actcatgtca	gtcctttgtg	attactgatt	240
attattattc	cccannnnnn	nnnnnnnnn	nnnnnnnn	nnnnnnnnn	nnnnnnnnn	300
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<210> 214 <211> 425 <212> DNA <213> Homo sapiens

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<210> 215 <211> 608 <212> DNA <213> Homo sapiens

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<210> 216 <211> 858 <212> DNA



## <213> Homo sapiens

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<210> 217

<211> 399

<212> DNA

<213> Homo sapiens

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752

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<210> 222

<211> 489

<212> DNA

<213> Homo sapiens

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<211> 493

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<213> Homo sapiens

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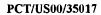
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<211> 420

<212> DNA

<213> Homo sapiens

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<212> DNA

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<213> Homo sapiens

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<213> Homo sapiens

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<210> 238

<211> 739

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<210> 240 <211> 1090 <212> DNA <213> Homo sapiens

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<210> 241 <211> 680 <212> DNA <213> Homo sapiens

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<210> 242 <211> 491 <212> DNA <213> Homo sapiens

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<210> 243

<211> 983

<212> DNA

### <213> Homo sapiens

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ctgcccatcg tggacaaggg ccccgtggag ctgctggagg agttcgtgtt ccaggtgccc
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aaggagcgca gcgcgcagcc caagagactg aattcccttc aggagcttca acttcttgaa
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                                                                     360
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                                                                     480
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                                                                     540
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ttctgctgcc agttcatcac ctccgttacc gcgctctatg acctgtcatc agatgacctc
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gtggggatgg acagagactc ccacctcttg tactcaaaac tccacctcag cgtcctgcaa
                                                                     900
                                                                     960
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gatcctcttc gaccacatgg tcc
                                                                     983
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<212> DNA
<213> Homo sapiens
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<210> 244

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cctgtactac gacggctgtg ccatgatcgc catgaacgga agcgtctttg ctcaaggatc
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                                                                     240
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gagetacagg geggagattt catetegaaa eetggeggtg agtgeteeag tagacacetg
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                                                                     360
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ggggetggtg ccgcagacag aacctgctte catctgttee ccgtcatcet ctgcttggge
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<210> 245 <211> 418 <212> DNA , <213> Homo sapiens

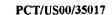
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	ggtgtctaca					300
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<210> 246 <211> 706 <212> DNA <213> Homo sapiens

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<210> 247 <211> 439 <212> DNA <213> Homo sapiens

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<210> 248 <211> 730

<212> DNA

<213> Homo sapiens

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<210> 249

<211> 466

<212> DNA

<213> Homo sapiens

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gttgccctcg aagatacaag cccttcaacg cccgctataa actgctgatc cacatgagag	180
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agcatceggg ttgtcagaag gccttcagta actccagtga cegegecaaa caccagegga	360
cgcatctgga cactaaacct tatgcttgtc aaattccagg atgtaccaaa cgctacacag	420
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<210> 250

<211> 963

<212> DNA

<213> Homo sapiens

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acaccages.	cccaccatca	cagtcgccac	cacctcagtc	catcettggt	accggcaatg	240
geacecagae	cotoceatac	acttgtaact	gacttggaca	cggaatacta	agaactcact	300
ggettegtat	tecceagege	accegeace	accet ot caa	ctcttttaga	cttaactgcc	360
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gctcctctgg	actctgtctg	actttggggg	caccarggac	caaagtggga	eggagaceee	
tataaccctc	atcattaaag	caccgaatca	gaaatacagt	gaccagacta	ttagetgett	480
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agraagrary	caaaagctgg	5550050050	to a to a a t	aggretettt	taataaacca	660
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cgaggtattt	tgagttctga	ggttgtgtct	cctgagtgtt	cgaaccatca	ttaatatttt	720
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gcgggcggat	cacgaggtca	ggagttcgag	accagecca	ccggcacggc	gaaaccccgc	
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tcq	,		. 11			963

<210> 251 <211> 894 <212> DNA <213> Homo sapiens

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<210> 252 <211> 861 <212> DNA <213> Homo sapiens

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180
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556

WO 01/53455

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atttgttctc	attcaacttg	tccagagggt	ttcaatgtct	ttgtgtaaat	ggtttacata	660
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tgaaaattaa	ggtatgattt	cagtgaaaag	taccaagtgt	tgtattgtgc	gaaggaaaag	780
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<210> 253

<211> 556

<212> DNA

<213> Homo sapiens

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<210> 254

tccagttaaa gaatag

<211> 435

<212> DNA

<213> Homo sapiens

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<210> 255 <211> 698 <212> DNA

<213> Homo sapiens

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<210> 256 <211> 736

<212> DNA

<213> Homo sapiens

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<210> 257

<211> 77

<212> DNA

<213> Homo sapiens





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<210> 260

<211> 414

<212> DNA

<213> Homo sapiens



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tcttaaatca	ctqqqqaaqq	gaatgataca	acatttcaga	cacatagttt	ccctagttta	240
		taaatacata				300
~ ~	_	ttgctgtctg	_			360
		aaaggaggta		_		414

<210> 261 <211> 620 <212> DNA

<213> Homo sapiens

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<210> 262 <211> 418 <212> DNA <213> Homo sapiens

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ttgccaagca agccatgttt tcaaggcacc cagggatgag gaagtggcct cgtcaatatg 360
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<210> 263 <211> 441

<212> DNA

<213> Homo sapiens

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<210> 264

<211> 832

<212> DNA

<213> Homo sapiens

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	gacccagcaa					=
gtgacgacgt	ccaccgctcc	cgccatggcc	tcagcctcca	ggaccaaatg	gagaggaagg	240
ccatttacgg	ccccaacgtg	atcagcatac	cggtcaagtc	ctacccccag	ctgctggtgg	300
	cagcatcgcg					360
	ttcctccatc					420
	ggacatggtc					480
	ggtggactcc					540
	gatgccctgt					600
	aggagagagc					660
	agagacacac					720
	tgtgggaccg					780
	tgagagagat					832

<210> 265

<211> 714

<212> DNA

<213> Homo sapiens



1860 1872

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	gtggagcgga					180
	cccaatgcca					240
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tccatacaac	gagtccttcc	cggttccaga	cccctcggtg	gcccaggtgc	tggtggagca	360
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<210> 266 <211> 1872 <212> DNA <213> Homo sapiens

<400> 266

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<211> 684 <212> DNA

<213> Homo sapiens

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<210> 268

<211> 453

<212> DNA

<213> Homo sapiens

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<210> 269

<211> 525

<212> DNA

<213> Homo sapiens

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ggggggtgc acgtctttaa tcccagctac tcagggcggg ggccaggggg tggggtaggg 180
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aataaataga taaataaaat aaaataaaat aaaaagaact cgaccctttt tacaatagct 360 aaaggaaaat aaaatactta agaataact taaccaagga ggtgaaagac ctctacaaag 420 aaaactacaa aacactgctg aaagaaatca cagatgacac aaacaaaaac acatcccaag 480 ctcatggaca ggtagaatca atactgtgaa aatgactata ctgcc 525

<210> 270
<211> 880
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (1)...(880)
<223> n = a,t,c or g

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<210> 271 <211> 1066 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (1) ... (1066) <223> n = a,t,c or g



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<210> 272

<211> 659

<212> DNA

<213> Homo sapiens

<400> 272

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aacaacccca	gggtcacacc	cctgctgatg	tacagcgacc	ttggctacgt	catccatggg	600
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<210> 273

<211> 412

<212> DNA

<213> Homo sapiens

<400> 273

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<210> 274 <211> 522 <212> DNA <213> Homo sapiens

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<211> 650 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (1)...(650)

 $\langle 223 \rangle$ n = a,t,c or g

<210> 275

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<210> 276 <211> 497 <212> DNA <213> Homo sapiens





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<210> 277 <211> 428

<212> DNA

<213> Homo sapiens

<400> 277

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	agcctcaaga					420 428

<210> 278

<211> 427

<212> DNA

<213> Homo sapiens

<400> 278

11007 21	•					
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ctggctccca go	ctggttgt gg	cagggctc	tctgcccaca	gggaggtagc	ccagttctgc	180
ttcacacact gg						240
agtgggggtg ta						300
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<210> 279

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<211> 561

<212> DNA

<213> Homo sapiens

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<211> 792

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<213> Homo sapiens

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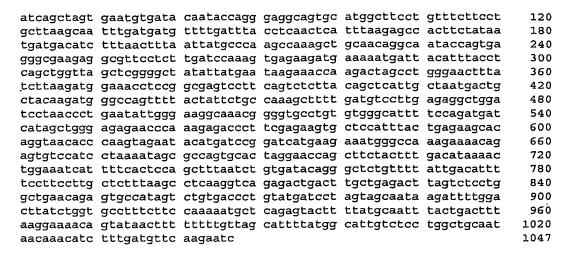
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<213> Homo sapiens

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<210> 282 <211> 357 <212> DNA

<213> Homo sapiens

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atgaggaatt cctttttcct gataaaaaag atagacaaaa tagtgagaga gaagctggaa 180
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tgcatatagt aacactctta ctaccacagt tatctcactt cttttgtctt agaatagaaa 300
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<210><211><212><213>	440	: ns				
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<210> 288
<211> 100
<212> DNA
<213> Homo sapiens
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tagcacaaat	cccctctag	agtgtcatgt	tggttgggta	atggattcca	gagaccatgg	180
gccaggaaca	tcctctgtca	gcacttcaaa	tgcttcacct	tcagaaggcg	caccactage	240
aggaagttat	ggatgtactc	ctcattcatt	cccaaagttc	cagcatcctt	ctcatgaact	300
tttgaaggaa	aatggcttta	cccaacaagt	gtaccacaag	tatcgtcgaa	gatgcctaag	360
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<210> 290 <211> 359 <212> DNA <213> Homo sapiens

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<210> 291 <211> 954 <212> DNA <213> Homo sapiens

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<210> 292 <211> 595 <212> DNA <213> Homo sapiens

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<210> 293

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<210> 294 <211> 426 <212> DNA <213> Homo sapiens

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	tgctcgctgg			55-55-55	34-0555405	217
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	gatgcagatt					240
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	tctggcggaa					420
	caccgtttgc					480
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120

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<400> 303

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ctgatgcgca gcgaattgcg tgagatcccc ccacacgact ggggtaaaac tctgaaagag 180
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gatatttcca tgcaccgact gcgtggcggc gaaattgtcg ccctggacga tcagtacacg 300
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<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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ataa						304

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<211> 344

<212> DNA

<213> Homo sapiens

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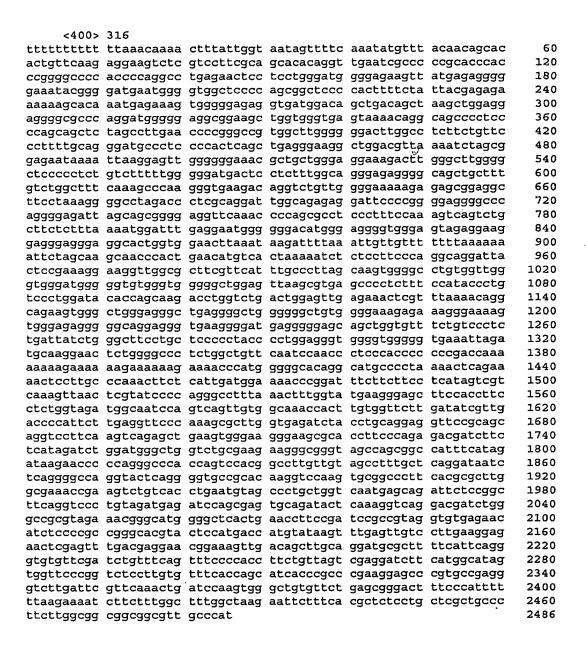
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PCT/US00/35017 WO 01/53455

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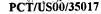
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<210> 327

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<212> DNA



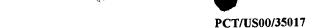
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<213> Homo sapiens

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WO 01/53455

<213> Homo sapiens

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<213> Homo sapiens

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<211> 5654
<212> DNA
<213> Homo sapiens
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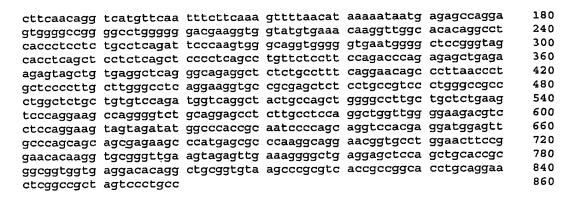
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<213> Homo sapiens

<400> 344

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                                                                     120
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aatgagaaac aaatgtcaac ataataaaat ctcagttaaa atacttgaaa aattcttaac
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<210> 345

<211> 1253

<212> DNA

<213> Homo sapiens

<211> 419

<212> DNA

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<213> Homo sapiens

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<210> 347

<211> 918

<212> DNA

<213> Homo sapiens

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<210> 350 <211> 1062 <212> DNA <213> Homo sapiens <220> <221> misc_feature <222> (1)...(1062) <223> n = a,t,c or g

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	ggggatcctt					300
	ggaaaactgg					360
	tggaagtgtg					420
	tgcaggcaag					480
	gagccttctg					540
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	gcctcccacc					660
	catcctcttt					720
	aggagagatc					780
	catttccctt					840
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<210> 352

<211> 1194

<212> DNA

<213> Homo sapiens

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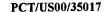
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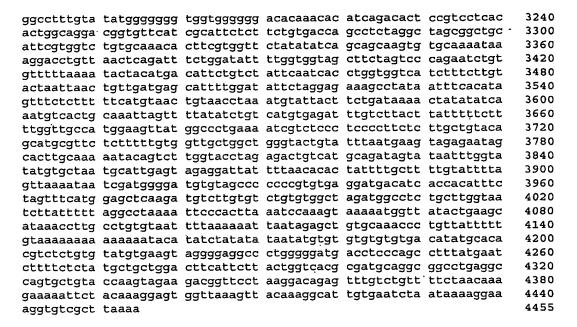
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WO 01/53455 PCT/US00/35017

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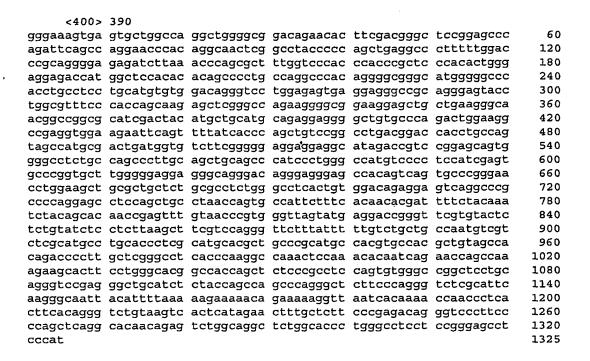
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<212> DNA

<213> Homo sapiens



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<212> DNA
<213> Homo sapiens
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<211> 1938

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<223> n = a,t,c or g
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<211> 1283

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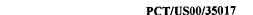
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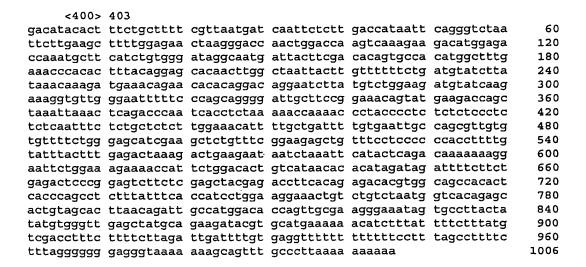
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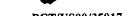
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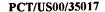
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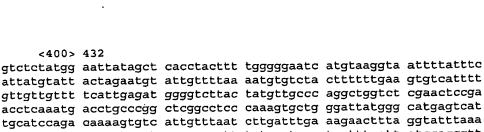
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WO 01/53455

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<211> 1102

<212> DNA

<213> Homo sapiens

<400> 441

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<213> Homo sapiens

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<210> 443

<211> 458

<212> DNA

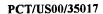
<213> Homo sapiens

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<210> 444

<211> 1681

<212> DNA



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		ggtactcgtg				780
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		ttacaagggc				960
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acaaccatga aatetgtegt gtgcaaaatg aaccccatga ctgacgegge ttcctgeggt
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                                                                     540
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<211> 468

<212> DNA

<213> Homo sapiens

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<210> 447

<211> 1030

<212> DNA

<213> Homo sapiens

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	cgtcagcgaa					480
	gccaaggaga					540
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	cgcttcttgc					780
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<210> 448

<211> 1936

<212> DNA



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<210> 449
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<213> Homo sapiens

<400> 449

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<210> 450

<211> 1073

<212> DNA

<211> 354

<212> DNA



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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

<400> 453

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WO 01/53455

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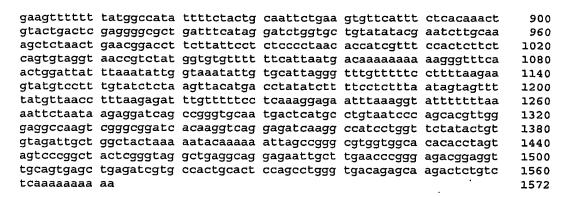
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3652

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<211> 2477

<212> DNA

<213> Homo sapiens

<220>

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